

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
1 April 2004 (01.04.2004)

PCT

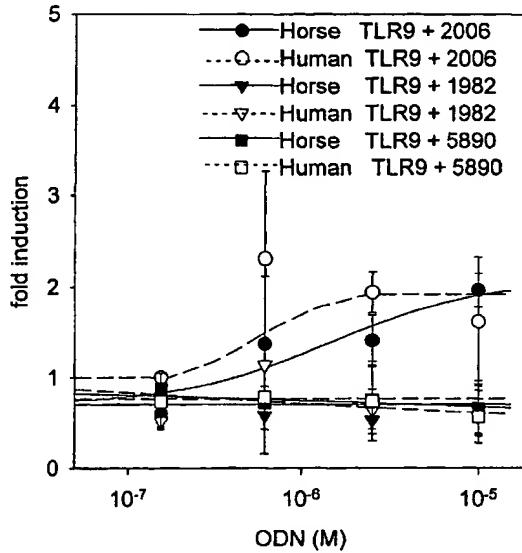
(10) International Publication Number
WO 2004/026888 A2

(51) International Patent Classification⁷: C07H
(72) Inventors; and
(75) Inventors/Applicants (for US only): LIPFORD, Grayson, B. [US/US]; 38 Bates Road, Watertown, MA 02472 (US). MOOKHERJEE, Neeloffer [IN/CA]; Apt 408, 2233 Allison Road, Vancouver, BC V6T 1T7 (CA). BABIU, Lorne [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). BROWNLIE, Robert [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). GRIEBEL, Philip [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). MUTWIRI, George [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). HECKER, Rolf [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).

(21) International Application Number: PCT/US2003/029577
(22) International Filing Date: 19 September 2003 (19.09.2003)
(25) Filing Language: English
(26) Publication Language: English
(30) Priority Data: 60/412,479 19 September 2002 (19.09.2002) US
(71) Applicants (for all designated States except US): COLEY PHARMACEUTICAL GMBH [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). UNIVERSITY OF SASKATCHEWAN [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). QIAGEN GMBH [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).
(74) Agent: STEELE, Alan, W.; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).
(81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.

WO 2004/026888 A2



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES**Background of the Invention**

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory 5 CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001) *Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for biological activity and it is reported that optimal CpG DNA sequences can vary among species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

10 Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN. Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9 recognizes CpG DNA is not understood.

Summary of the Invention

15 Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal in response to CpG DNA. To date, the amino acid sequences only of human and murine TLR9 have been reported, and, interestingly, these two species are known to prefer different CpG motifs. The structural basis for this species-specific CpG motif preference has not yet been fully elucidated. The instant invention provides, in part, novel amino acid and 20 nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are useful for elucidating certain key structural features of TLR9. Specifically, comparison of sequences of murine, human, and these novel TLR9 sequences permits identification of areas of highly conserved sequence, areas of group conservation, and areas of hypervariability. In addition, such comparisons permit an assessment of evolutionary relatedness among TLR9 25 molecules of the various species, as well as an assessment of inter-species homologies. Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9 that may be involved in the CpG binding site, as well as amino acids involved in conferring species specificity for particular CpG motifs. Such information may be used to design and construct novel TLR9 molecules which incorporate specific point or regional mutations and 30 which possess desired ligand binding characteristics. Such information may also be useful in designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an 5 extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

10 In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand, 15 such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID 20 NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid 25 molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the 30 invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third 5 species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate 10 amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively 15 with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino 20 acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an 25 amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of 30 the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment 10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide 15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in 20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

TCCATGACGTTTTGATGTT	(SEQ ID NO:39),
TCCATAACGTTTTGATGTT	(SEQ ID NO:40),
TCCATCACGTTTTGATGTT	(SEQ ID NO:41),
25 TCCATTACGTTTTGATGTT	(SEQ ID NO:42),
TCCATGGCGTTTTGATGTT	(SEQ ID NO:43),
TCCATGCCGTTTTGATGTT	(SEQ ID NO:44),
TCCATGTCGTTTTGATGTT	(SEQ ID NO:45),
TCCATGATGTTTTGATGTT	(SEQ ID NO:46),
30 TCCATGAAGTTTTGATGTT	(SEQ ID NO:47),
TCCATGAGGTTTTGATGTT	(SEQ ID NO:48),
TCCATGACATTTTGTGTT	(SEQ ID NO:49),
TCCATGACCTTTGATGTT	(SEQ ID NO:50),
35 TCCATGACTTTTGTGTT	(SEQ ID NO:51),
TCCATGACGTTTTGATGTT	(SEQ ID NO:52),
TCCATGACGATTTGATGTT	(SEQ ID NO:53),
TCCATGACGGTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTGATGTT (SEQ ID NO:55),
TCCATGACGTATTGATGTT (SEQ ID NO:56), and
TCCATGACGTGTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes
5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one
embodiment the reporter gene is operatively linked to a promoter sensitive to NF- κ B. In one
embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or
CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test
10 compounds. In one embodiment the response mediated by the TLR9 signal transduction
pathway is measured quantitatively and the response mediated by the TLR9 signal
transduction pathway associated with each of the plurality of test compounds is compared
with a response arising as a result of an interaction between the functional TLR9 and a
reference immunostimulatory compound.

15

Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid
sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig
(porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid
20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9
polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and
1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six
sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and
human TLR9 sequences alone.

25

Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine,
porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected
oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30

Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9
derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key
features of the primary sequences of these and related TLR molecules, including previously

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands.

5 Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as 10 to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may 15 represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from 20 the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See 25 Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on 30 comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9

10 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

15 An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9

(See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAELALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI
 5 HHLHNLDVFVHLPNVRQLNWKWCNCPPGSLPHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
 SHTNIVLVDASSLAGLHSLRVLFMMDGNCYYKNPCNGAVNVTDAFLGLSNLTHLSLKYNNLTEVPRQLPPSLEYL
 LLSYNLIVKLGAEIDLNLTSRMLDVGNCRRCDHAPDLCTECRQKSLDLHPQTFHLSHLEGLVLDSSLHSLN
 SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDLSFNYCKKVSFARLHASSFKSLVSLQELNMNGIF
 FRLLNKNTLRLWLAGLPKLHTLHQMFINQAQLSVFSTFRALRFVDSLNNRISGPPTLSRVAPEKADEAEKGVPW
 10 PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
 VLDLSYNIKLDLYHSKSFSELPQLQALDLSYNSQPFMNGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
 VEYLDFSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSQNKLHILRPQNLNYLPKSLTKLSFRDNHLSFFNWSSLA
 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
 MNLTVDVSSNPLHCACGAPFVDSLLEVQTKVPGLANGVKCGSPQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL
 15 AVAVGTVLPLLQHLCGWDVWYCFHLCIWLPLLTRGRRSAQALPYDAFVVFDAQSAVADWVYNELRVLEERRG
 RRALRLCLEDRDWLPGQTLFENLWASIYGSRKTLFVLAHTDKVSGLLRTSFLAQQLLEDRKDVVVLVILRPDA
 HRSRYVRLRQLCRQSVLFWPQNGQGSFWAQLSTALTRDHHFYNRNFCRGPTAE

SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAELALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAEPRSNITSLSLIANRI
 20 HHLHNLDVFVHLPNVRQLNWKWCNCPPGSLPHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
 SHTNIVLVDASSLAGLHSLRVLFMMDGNCYYKNPCNGAVNVTDAFLGLSNLTHLSLKYNNLTEVPRQLPPSLEYL
 LLSYNLIVKLGAEIDLNLTSRMLDVGNCRRCDHAPDLCTECRQKSLDLHPQTFHLSHLEGLVLDSSLHSLN
 SKWFQGLANLSVLDLSENFLYESINKTSAFQNLTRLRKLDLSFNYCKKVSFARLHASSFKSLVSLQELNMNGIF
 FRLLNKNTLRLWLAGLPKLHTLHQMFINQAQLSVFSTFRALRFVDSLNNRISGPPTLSRVAPEKADEAEKGVPW
 25 PASLTPALPSTPVSKNFMVRCKNLRFTMDLSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
 VLDLSYNIKLDLYHSKSFSELPQLQALDLSYNSQPFMNGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
 VEYLDFSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSQNKLHILRPQNLNYLPKSLTKLSFRDNHLSFFNWSSLA
 FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
 MNLTVDVSSNPLHCACGAPFVDSLLEVQTKVPGLANGVKCGSPQLQGRSIFAQDLRLCLDDVLSRDCFG

30

SEQ ID NO:3 (Rat TLR9)

atggttctctgtcgcaggaccctgcacccttgtctctcctggtagccgcaggctggctgaggctctggcc
 ctgggtaccctgcctgccttccatccctgtgaactgaagcctcatggcctggtagactgcaactggctttcctg
 aagtctgtgcctcacttctgtccgcagaaccccttccaacatcaccagccttccttgcacgcataccgcac
 35 caccacactgcacaacctcgactttgtccacctgcacgcacactgtaacactcaagtggaaactgtccgccc
 cctggcctcagcccttgcacttctctgcgcacattgagccaaaaccccttgcctatgcacatgctg
 gaagagctgaacctgagctataacggtatcaccactgtccccgcctgcccacgccttgcacgaatctgagccta
 agccacaccaacatcctgtactcgatgccagcgcctgcgtggcctgcacgcctgcgagttcttcatggac
 gggactgtactacaagaacccctgcaacggggcgtgaacgtgacccggacgccttctggcttggcaac
 40 ctcacccacttgtcccttaagtataacaacctcacagagggtgccccgcaactgccccccagcctggagttac
 ctgctgtcctataacctcatcgtaagctggggccaaagacactgccaactgcaccccttcgaatgtcttgc
 gtgggtggaaattgcgtcgctgtatcagccccgacctctgtacagaatgcggcagaagtcccttgcac
 caccctcagacttccatcacctgagccaccccttgcggactgtggcgtgacccactcgctgaaac
 45 tccaagtggttccagggtctggcgaacctctcggtgtggacctaagcgagaacttcttgcac
 aaaacccaggcccttcagaacctgacccgtcgcaagctcgacactgtccctcaattactgcaagaaggat
 ttcgccccctccacctggcaagttcttcaagagcctggctgtcgctgcaggagctgaacatgaacggcat
 ttccgcgttactcaacaagaacacgcgtcagggtggctgtggctggccaaagctccacacgcgtgcac
 aatttcatcaaccaggcgcaagctcagcgtcttttagtacccctcgagcccttcgccttgcggac
 50 cgcacatcagcggccctccaaacgcgttccagactgtcccgatgcggccaaaaggcagacgaggcggaga
 cctgcaagtctcaccctccaggactctcccgactccgtctcaaaaacttcatggctcagggtgaa
 ttcaccatggaccctgtctcgaaacaaccagggtactatcaaggccagagatgttgcgtcaacc
 tccatctccatcgatgcgtcaggctgtcaatggctctcaggcttcgtccgcgtgaccaac
 tggctggaccctgtctataacaagctggaccattcgaaatcgatcgactggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaactcagtttctggccaatctg
 tccaggttacagaacaccttagctggcacacaatgacattcacagccgcgtgcctcacgcctcacagcacctca
 gtggagtatctggacttcagccgcaacggtgtggccgcatactggacgaggaggaccttaccttacccatcttc
 5 caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggcccaacgcacccat
 tacctcccaagagcctgacgaagctgagttccgtgacaatcacctctttaactggagcagtctggcc
 ttccctggcaatotgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta
 ggcacgcctccagaaactggatgtcagtagcaacagttatcgtcttgcattgtgcctgcgggcaccccttgc
 10 gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatgcctcgcgggttggccatgtg
 atgaacctgacggttctagacgtgagcagcaaccctctgcattgtgcctgcgggcaccccttgc
 ctggaaagtgcagaccaaggtgcctggcgtcaacgggtgtgaagtgtggcagtccccggcagctgcaggccgc
 agcatcttgcgcaagacactgcggctgtgcgttgcattgcacgcatttcgcggactgccttgcactcctg
 gctgtggccgtggcacgggtgtgccttactgcacatctcgcggctggacgtctggactgtttccatctg
 tgcctggcatggctaccccttgcattgcacccgtggccggcgcagcccaagctcccttatgcattgccttc
 15 tgcataaggcgcagagcgcgggtgtcactgggtgtataacgcagttcgcattgcggcttagaggagcggcgc
 cggcagccctacccgtgtggaggaccgagattggcgtgcctggccagacacttcgcgaaacctctggcc
 tccatctatggcagccgcacagactctgttgcattgcctccacacggacaaggcattgcgcaccgc
 ttccctgtggctcagcgcgcctgtggaggaccgcaaggacgtgggtgttgcattgcgcctgtatgc
 caccgcctccgcatacgtgcactgcgcacgcctgcgcgcctgcgcgcagactgtgttgcattgc
 20 gggcaggccagctctggcccaagctgagtagcgcactgcattgcattgcggacaaccaccacttataacc
 tgccggggacctacagcagaatag

SEQ ID NO:4 (Rat TLR9)

atggttctctgtcgcaggacccctgcacccttgcattctcctggtacaggccgcagtgcctggctgaggctctggcc
 ctgggtaccctgcctgccttccatccctgtgaactgaagcctcatggcctgttagactgcacactggcttccctg
 25 aagtctgtgcctcacttctctggcgcagaacccctgttccacatcaccagccttccttgcattgcacccgcac
 caccacctgcacaacccctgactttgtccacctgcacacgtgcgcacagactgcacacttgcattgcgc
 cctggcctcagcccttgcacttctcgcgcattgaccattgcacccaaacccctgcattgcgcattgcgc
 gaagagctgaacctgagctataacggtatcaccactgtgcctgcgcgcctgcgcgcagacttgc
 30 agccacaccaacatccgttactgcattgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
 gggactgcactacaagaacccctgcacggggcgtgaacgtgcacccgcgcgcgcgcgcgcgcgc
 ctcaccactgtcccttaagtataacaacactcacaagggtgcgcgcgcgcgcgcgcgc
 ctgcgtgcctataacactcatgcattgcacactgtggggccgcacactgcattgcattgcattgc
 gtgggtggaaattggcgtcgctgttgcattgcacgcgcgcgcgcgcgcgcgcgc
 35 caccctcagacttccatcaccctgagccaccccttgcattgcattgcattgcattgcattgcattgcatt
 tccaaagtggttccagggtctggcgcacccctcggtgcattgcattgcattgcattgcatt
 aaaaccaggcgccttcagaacactgcacccgtctgcgcacactgcattgcatt
 ttgcgcgcctccacccctggcaacttgcattgcattgcattgcattgcattgcatt
 ttccgcattactcaacaagaacacgcctagggtggctggctggctggcc
 40 aatttcatcaaccaggcgcacgcctcgcattgcattgcattgcattgcatt
 cgcattgcgggcctccaaacgcctgcattgcattgcattgcattgcatt
 cctgcattgcattgcattgcattgcattgcattgcattgcattgcatt
 ttacccatggacccctgcattgcattgcattgcattgcattgcatt
 tgcattgcattgcattgcattgcattgcattgcattgcattgcatt
 45 gtgcattgcattgcattgcattgcattgcattgcattgcattgcatt
 ctggacactgagctacaacagccagccattcagcatgcattgcatt
 tccaggttacagaacacttagctggcattgcattgcattgcatt
 gtggagtatctggacttcagccgcaacggtgtggccgcatt
 50 caagacctgagaagcctgattcatctggacctgtctcagaata
 taccccttgcattgcattgcattgcattgcattgcatt
 ttccctggcaatctgcgagacactggcattgcattgcatt
 ggcacgcctccaggaaactggatgtcattgcattgcatt
 gtagagctaaaagaggtcaacccctcagccataacatc
 atgaacctgacggttctagacgtgagcagcaaccct
 ctggaaagtgcagaccaaggtgcctggcattgcatt
 55 agcatcttgcgcaagacactgcggctgtgcattgcatt
 gacgcattgcattgcattgcattgcattgcatt

- 11 -

SEQ ID NO:5 (Porcine TLR9)

5 MGPRTCLHPLSLLVQVTALAAAQGRLPAFLPCELQPHGLVNCNWLFLKSVPFSAAPRANVTSLSLLSNRIH
HLHDSDFVHLSSLRLTNLKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNSYNSTITVPALPDSDLVSLSLS
RTNILVLDPTHLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSSLKYNLLEVPRSLPPSLETLL
LSYNHIVTLLTPEDLANLTALRVLDDVGGNCRRCDHARNPCRECPKDHPKLIHSDFSHSLRLEGVLKDSSLNLDT
RWFRLDRLQVLDLSENFLYDCITKTITAFQGLARLRLSLSNLFNYHKKVSAFHLLAPSGHRLSLKEELDMHGIFF
RSLSETTLQPLVQLPMLQTLRLQMNFIQQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDRERVWLPSR
NLAPRPLDTRLSEDIFMPNCKAFSFTLDSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSRLV
DLSHNKLDLYHGRSFTELPRLAEALDLSSYNSQPTMCGVGHNLSFVAQLPALRYLSSLAHNDIHSRVSQQLCSASL
10 ALDFSGNDLSRMWAEGDLYLRRFFQGLRSLVWLDSQNHLHTLLPRALDNLPKSLKHLHLRDNLIAFFNWSSLTLL
PKLETLDLAGNQNLKALNSGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSVMGN
LKVLDSANPLHACGATFVGFLLEVQAAVPGPLPSRVKCGSPGQLOQHSIFAQDRLRLCDETLSWNCFGISLLAM
ALGLVVPMLHLCGWDLWYCFHLCIAWLPHRGQRRGADALEPYDAFVVFDKAQSAVADWVYNELRVQLEERRGRRA
15 LRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLRASFLLAQQRLLEDRKDVVVLVILRPDAYRS
RYVRLRORLRCROSVLLWPHOPRGOGFSWAOLGTALTRDNHHFYNRNFCRGPTTAE

SEQ ID NO:6 (Porcine TLR9)

20 MGPRTCLHPLSLLVQVTALAAAALAQGRLLPAFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRANVTSLSLLSNRIH
HLHDSDFVHLSSLRTLNLKWNCPAGLSPMFPCMHMTIEPNTFLAVPTLEELNSYNSITTVPALPDSLVSLSLS
RTNILVLDPTHLTGLHALRYLYMDGNCYYKNPCQGALEVVPGALLGLGNLTHLSLKYNNLTEVPRSLPPSLETLL
LSYNHIVTLPEDLANLTALRVLDDVGGNCRRCDHARNPCRECPKDHPKLNHSDFSHSLRLEGVLVKDSSLYNLDT
RWFRLGLDLRQLVLDLSENFLYDCITKTTAFQGLARLRLSLSNLSFNYHKVVSFAHLHLAPSFGHLRSLKELDMHGIFF
RSLSETTLQPLVQLPMLQTLRLQMNFINQQAQLSISFGAFTPGLLYVDSLSDNRISGAARPVAITREVDGRERVWLPSR
NLAPRPLDTLRSDFMPNCKAFSFTLDLSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTLSRVL
25 DLSHNKLDLYHGGRSFTELPRLEALDLSYNSQPFMMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC
ALDFSGNDLSSRMWAEGDLYLRFQGLRSVLWLDLSQNHLHTLLPRALDNLPKSLKHLHRLDNNLIAFFNWSSLTLL
PKLETLDLAGNQLKALSNGLSPSTQRLRDLGSNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFSGSMVGN
LKVLDDVSANPLHACGATFVGFLLEVOAAVPGPLPSRVKCGSPGOLOGHSIFAODLRLCLDETLWSWNCFG

30 SEQ ID NO:7 (Porcine TLR9)

35 gggcaggctgcctgccttcgtgcagccacggcctgtgactccagccacggcctgtgactcaactggcttcctgaa
gtccgtccccacttctcgccggcagcggccacggcactcaccagccttcctactctccaaccgcatccaa
ccacctgcacgactccgacttcgtccacctgtccagcctacgaactctaaccctaagtggaaactgcccgcggc
tggcctcagccccatgcacttccctgccacatgaccatcgagccaaacaccccttgcggctgcccacccttggaa
ggagctgaacctgagctacaacagcatcacgaccgtgcctgcctgcccactccctcgtgtccctgtcgctgag
ccgcaccaacatcctggctagaccccccacccacctcactggcctacatgcctgcctacactgtacatggatgg
caactgctactacaagaacccctgcagggggcgtggagggtggccgggtccctcctggccctggcaaccc
40 cacacatctctcactcaactcaagaacatctcacggaggtggccggcagcctgcctggagacccctgtc
gttgcctacaaccacattgtcacccctgacgcctgaggacctggcaatctgactgcctgcgtgtatgt
gggggggaaactgcccggctgtgaccatgcccgaacccctgcagggagtgcccaaaggaccacccaaagctgca
ctctgacacccctcagccacctgagccgcctcgaaggcctgtgtgaaagacagttctctacaacactggacac
45 caggtggttccgaggcctggacaggcgtcaagtgtggacctgtgactgtgagaacttcctctacgactgcaccaaa
gaccacggccctccaggccctggccactgcgcagcctcaacctgtcctcaattaccacaagaagggtgtcctt
tgcccacctgcacctggcaccccttggcacctccggcccttgcggacatgcattggcatcttctt
ccgctcgctcagtgagaccacgcgtccaaacctctggcccttgcggacatgcctatgcctccagaccctgcgcctgcagatgaa
cttcattaaaccaggcccaagctcagcatcttggcccttgcgtgtacgtggacctatcgaccaacc
catcagcggagctgcacaggccactgtggccattacttagggaggtggatgttggagagggtctggctgccttccag
50 gaacctcgctccacgtccactggacactctccgtcagaggacttcatgcacccactgtcaaggccctcagctcac
cttggacctgtctcggaacaacctgtgtacaattccagtcggagatgttgcctgccttcacgcctcgagtgcc
gcccgcgtgaccacacgcgtccacggccgtcaatggcttcagttgtgcctgcgtaccagccctgcgggtgt
ggacacctgtcccaacaagaactggacactgtatcacggccgtcgttacggagctgcgcgcctggaaagcactggaa
cctcagctacaatagccaccccttaccatqcaqqqtgtqcccaacaacctcaqctcgtqcccaqctqcccc

- 12 -

5 cctgcgctacccatcgccctggcgccacaatgacatccatagccaggtgtcccagcagctctgttagccctcaactgtgcggcgtttagcgccaaacgatctgagccggatgtgggtgagggagaccttatctccgttccaaagg
cctaagaagcctagtcgtggactgtcccaagaaccacccatgcacaccctctgtccacgtgcccggacaacccat
ccccaaaagcctgaagcatctgcattccgtgacaataaccctggcttcaactggagcagcctgaccctccat
5 gccaagcgtggaaaccctggacttggtggaaaccagctgaaggccctaagcaatgcagcctgccatctggcac
ccagctcgaggcgtggacccatcagtgcaacagcatcggtttgtgaaccctggcttgcctggccaagca
gttagaagagctcaacccatcagcgccaaatgcctcaagacagtggagccctctgtggctgatggggca
cctgaaagtcttagcgtgagcgccaaaccctctgactgtgcctgtggggcgacccctgtggcttgcctgg
ggtagcaggctggctggctggctggcccgccgtcaagtggtggcagtcggggcagctccaggccatagcat
10 ctttgcgcacagacccatgcgcctctgcctggatgagaccctctgtggactgtttgcacatctgcgtgtggccat
ggccctgggctgggtgtggccatgtgcaccacccatgcgtggccgtggacccctgtgtactgttccacctgtgcct
ggcctggctggccaccggaggccagccgcagccggccggccgcagacccctgttcatatgtgccttcgtgttgcacaa
agctcagagtgctgtggccgactgggtgtacaacgagctggggcagctggggcagctggaggagccgtggccgc
actgcgcctgtgcctggaggagccgagactgggttacccatggcaagacgccttcgtggccctcagtc
15 cagcagccgcacagaccctgttgcgtggccacacggaccgtgtcagccgttgcgtgcctcgttgcctgt
ggccctggccgcgtggaggaccgcaggacgttgcgtgtactgtgttgcacccatgcctaccgc
ccgctacgtgcggcgtgcgcacccatgcgtggccaggtgtccctctgtggcccccaccagcccgccgtggccagg
cagttctggcccaagctggcgcacagccctgaccaggacaaaccaccacttctataaccggaaacttctgcgggg
ccccacgacagccgaatagcactgagtgacagcccgatgtcccaagcccccctggatggctctgcctgg
20 tgcccaacccatgttgcgtccacaccactgtctgttccctgttccccaccccccaccccgccatgt
aacatgtgcccataaaatgttacccggaggccaaagaaaaaaaaaaaaaaaaaaaaaa

SEQ ID NO:8 (Porcine TLR9)

SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAAALAEGLPFLPCELQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
 5 HLHDSDFVHLSNLRLVNLWNCPAGLSPMHPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSLIS
 HTSILVLGPTHFTGLHALRFLYMDGNCYYMNPCPRALEVAPGALLGLGNLTHLSKYNNLTEVPTRLPPSLDTLL
 LSYNHIVTLAPEDLANLTALRVLVDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLDKSSLKLEK
 DWFRGLGRLQVLQLDLSENFLYDITKTTIFNDLTQLRLNLSFNYHKKVSFAHLHASSFGSLVSLEKLDMHGIFF
 RSLTNITLQSLTRLPKLQSLHLQLNFINQALISIFGAFPSLLFVDSLSDNRISGAATPAAALGEVDSRVEVWRRLP
 10 GLAPGPLDAVSSKDFMPSCNLNFTLDSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
 LSHNKLDLYHGRSFTELPQLEALDLISYNQFSMQMVGHNLFSVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA
 LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLDNNLAFFNWSSLTVLP
 RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFVVRATRLIELNLSANALKTVDPFWGSLAGTL
 15 KILDV SANPLHACGAAFDVDFLLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLSDCFG LMA
 GLAVPMLHHLCGWDLWYCFHLCIAHLPRRRRQRGEDTLLYDAVVFDKVQSAVADWVYNELRVQLEERRGRRAL
 RLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQLLEDRKDVVVLVILRPAAYRSR
 YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGI ALTRDNRFYNRNFCRGPTTAE

SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAAALAEGLPFLPCELQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
 20 HLHDSDFVHLSNLRLVNLWNCPAGLSPMHPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSLIS
 HTSILVLGPTHFTGLHALRFLYMDGNCYYMNPCPRALEVAPGALLGLGNLTHLSKYNNLTEVPTRLPPSLDTLL
 LSYNHIVTLAPEDLANLTALRVLVDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLDKSSLKLEK
 DWFRGLGRLQVLQLDLSENFLYDITKTTIFNDLTQLRLNLSFNYHKKVSFAHLHASSFGSLVSLEKLDMHGIFF
 RSLTNITLQSLTRLPKLQSLHLQLNFINQALISIFGAFPSLLFVDSLSDNRISGAATPAAALGEVDSRVEVWRRLP
 25 GLAPGPLDAVSSKDFMPSCNLNFTLDSRNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
 LSHNKLDLYHGRSFTELPQLEALDLISYNQFSMQMVGHNLFSVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA
 LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLDNNLAFFNWSSLTVLP
 RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIPGFVVRATRLIELNLSANALKTVDPFWGSLAGTL
 KILDV SANPLHACGAAFDVDFLLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLSDCFG

30

SEQ ID NO:11 (Bovine TLR9)

ggaaagtgggcgccaagcataccctccctgcagctgcctcccaacctgccccccagaccctctggagaagccgcatt
 cccctgtcatggggccctactgtgcggccgacccctttctctctggtgccggccgactggcagccggcc
 tggccgagggcaccctgcctgcctgcctgtggatgcctccagccatggccggactggactgcactggctgt
 35 tccctgaagtctgtgcgcacccctggctggagccccccggccaatgtcaccgcctcccttaatctccaaacc
 gcatccaccacttgcactgactctgacttcgatccacccgtccacccatgcgggtcctcaacccatcaagtgaaactggc
 cggccggccgcctcagcccatgcacttccctgcgtatgaccatgcggccaaacacccttctggctgtgc
 ccctggaggagctgaacctgagctacaacggcatcacgaccgtgcctgcctggccagggtccctctgtgtccctgt
 40 cgctgagccacaccagcatctggctggatggcccccacttcacccgcctgcacccgcctgcgcgtttctgtaca
 tggacggcaactgtactacatgaacccctgcccggccctggaggtggcccccaggccgccttcotcgccctgg
 gcaacccatcgccacccgtgcgtcaagtacaacccatcaccgcggatggccgcctggcccaacccatccatggaca
 ccctgtgtgtccataccacattgtcaccctgcacccggaggacccatggccaaacccatggactgcctgc
 ttgacgtgggtggaaactgcgcgcgtgcgaccatgcggcaacccctgcaggatggccgtggatggccaaagaacttccca
 45 agctgcaccctgacacccttgcgttgcacccatgcggccgtcaaggccatggatggacttgcctgc
 tagagaagatgggtccgcgcctggggcaggctccaatgtcgttgcacccatggatggacttgcctctatgactaca
 tcaccaagaccaccatctcaacgcacccatgcggccgtgcgcacactcaacccatgccttcattaccacaagaagg
 tggccttcgcgcctccctgcacccatgcgttgcacccatgcggccgtgcgttgcacccatgcacccatgc
 tcttcgttgcgttgcacccatgcggccgtgcgttgcacccatgcggccgtgcgttgcacccatgc
 50 agctgaacttcatcaaccaggcccagctcagcatcttggggccttcggccatggccgtcttcgttgc
 acaaccgcacccatgcggccgtgcacccatgcggccgtgcgttgcacccatgcggccgtgcgttgc
 tgcccaaggggcctgcgtccaggccgcgtggacccgcgtcagctcaaaggacttcatgcacccatgc
 tcacccatggacccatgcgttgcacccatgcggccgtgcgttgcacccatgcggccgtgcgttgc
 gcctgcgcctgcacccatgcggccgtgcgttgcacccatgcggccgtgcgttgcacccatgc

- 14 -

5 tgctcgaccctgtcccacaacaagctggaccctgtaccatggcgctcattcacggagctggccgcagctggaggc
tggacctcagctacaacacagccaggcccttcagcatgcagggcgctggccacaacactcagttcgccgcagctgc
cctccctgcgtcacctcagccttcgcacaatggcatccacagccgcgtgtcacagaagctcagcagcgcctcg
tgcgccctggacttcagcggcaactccctgagccagatgtgggcccaggagacacttatctcgcttttca
aaggcttgaggaaacctggccagctggaccctgtccgagaaccatctgcacacccctctgcctcgacactggaca
acctgcccacagagcctgcggcagctgcgtctccggacaataacactggcccttcactggagcagcctgacc
tccggcccgctggaaaggccctggatctggcagggaaaccagctgaaggccctgagcaacggcagcctgcccctg
gcacatccggctccagaagctggacgtgagcagcaacagcatcggcttcgtgatccccggcttcgtccggcgca
ctcggtgatagacttaacctcagcggcaatggccctgaagacagtggatcccttcgtggacttcgttccatcg
ggaccctgaaaatcctagacgtgaggcacaaccgcctccactgcgcctgcggggcgcccttggacttcgttcc
tggagagacaggaggccgtgcccggctgtccaggcgcgtcacatgtggcagttccggccagctccaggcccg
gcacatcttcacacaggacacctgcgccttcgtggatgagacccttccttggactgccttggcccttcactgt
tggtggcgctggccctggcagtgccatgctgaccaccttgcggacttgcgttccacactgt
gtctggcccatggcccgacggcgccggcagccggcgaggacaccctgtctatgtgcgttgttcc
acaagggtgcagagtgcagtggctgattgggttgcataacgcgcgtccgcgtcagctggaggagcgcgggggg
ggcgcgtccgccttcgtccggaggagcgcgcgtccgcgttgcgcgttgttgcggcccgcc
tctacagcagccgcacagaccatgttgcgttgcgcgttgcgcgttgcgcgttgttgcggcccgcc
tgctggcccgacgcgcctgttggaggaccgcaggacgcgttgttgcgttgttgcgcgttgttgcggcccgcc
ggtcccgctacgtgcggcgtgcgcgcgttgcgcgttgttgcggcccgcc
aggtagtttctggccaaacctggccatagccctgaccaggacaaccgtcacttctataaccggaaacttctgg
ggggcccccacgacagccgaatagcacagactgtactggccag

SEQ ID NO:12 (Bovine TLR9)

- 15 -

SEQ ID NO:13 (Equine TLR9)

5 MGPCHGALQPLSLLVQAAMLAVALAQGTLPPFLPCELQPHGLVNCNWFLKSVPHFSAAPRDNVTSLSLLSNRI
HHLHDSDFAQLSNLQKLNWKNCPPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL
SRTNILQDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTVPRSLPPSLEYL
LLSYNHIVTLAPEDLANLTALRVLVDVGNCRRCDHARNPCVCPHKFPQLHSDFSHLSRLEGVLKDSSLYQLN
PRWFGRGLGNLTVIDLSENFLYDCITTKTAKFQGLAQLRRLNLSFNYHKKVSFAHTLAPSFGSLLSQELEMHGIF
FRSLSQKTLQPLARLPLMQLRQLYQLQMNFINQAOQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
RDLTPGPLDTPSSEDFMPSCKNLSFTLDSLRSNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV
10 LDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMSMRGVGHNLFSVAQLPTLRLYSLAHNGIHSRVSQQLCSTL
WALDFSGNSLSQMWAEGLYLRFFQGLRSLIRLQLSQQNRLHLLPCTLGNLPLKSLQQLRLRNNYLAFFNWSSTL
LPNLETLDLAGNQLKALSNGLSPSGTQLQRLDVSRSNSIIFFVPGFFALATRLRELNLSANALRTEEPSWFGFLAG
SLEVLDVSANPLHACGAAFVDFLLQVQAAVPGPLPSRVKCCSPGQLQGRSIFAQDILRLCLDKSLSWDCFGSLLLV
VALGLAMPMLHHLCGWDLWYCFHGLAWLPRRGWORGADALSYDAFVFDKAQSAVADWVYNELRVRLEERRGRR
15 ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDARR
SRYVRLRORLCROSVLFWPHOPSGOFRSFWAOLGMALTRDNRFHYNQNFCRGPTMAE

SEO ID NO:14 (Equine TLR9)

20 MGPCHGALQPLSLLVQAAMLAVALAQGTLPPFLPCELQPHGLVNCNWLFKSVPHFSAAPRDNVTSLSSLNSRHHLHSDFAQLSNLQKLNWKWCNCPAGLSPMHPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLILSRTNILQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNLTTVPRSLPPSLEYLLLSYHNIVTLAPEDLANLTLRVLVDGGNCRRCDHARNPCVCPHKFPQLHSDFSHLSRLEGLVLDKSSLYQLNPRWFGRGLGNLTVLDLSENFLYDCITKTAKFQGLAQLRRLNLSFNYHKKVSAHFTLAPSFGSSLSQELEMHGIFFRSLSQKTLQPLARLPMQLRQLYLMQMFNQAOQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
25 RDLTGPGLDTPSSEDFMPSCKNLSFTLDLSRNMLVTQPEMFQALSRQLCRLSHNSISQAVNGSQFVPLTSQVLQLDLQSHNKLDDLYHGRSFTELPRLEALDLSSYNSQFMSMRGVGHNLFSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSLLWALDFSGNSLSQLQWAEGDLYLRFQGLRSLIRLQLSQRNLLHTLLPCTLGNLPKSLQQLRLRNNYLAFFNWSLLTLPLNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFFVPGFFALATRLRELNLSANALRTEEPSWFGFLAGSIEVLDVSANPLIHCACGAAFVDFLLOVOAAVPGLPSRVKCGSPGOLOGRSIFAODIRLCLDKSLSWDCFG

SEO ID NO:15 (Equine TLR9)

- 16 -

5 aatggctcacagttcgccactgaccgctgcagggtctggacactgtcccaataacaaactggacactgtaccat
ggcgctcgttacggagctgcccgcactggaggccctggacactcagactacaacagccagccctcagcatgcgg
ggtgtggccacaacctcagttgtggccagctgcccacccctgcgctacctcagctggcacacaatggcattc
cacagccgtgtgtcccagcagctctgcagcacctcgctgtggccctggacttcagcggcaattccctgagccag
10 atgtggctgagggagacctctatctccgttcttccaaggcctgagaagcctaattccgctagacactgtccca
aatcgctcgatcacccctctgcccactgcacccctggcaaccccccacagagcttgcagctgcgtctccgtaa
aattacctggcccttcaattggagcagcctgaccctcctgcccacccctggaaaccctggacccctggctggaaac
cagctgaaggctctgagaatggcagcctgcctctggcacccagctccagaggctggacgtcagcaggaaac
atcatcttcgtggccctggcttcttgctctggccacgaggctgcgagagctcaacactcagtgccaaacgcctc
15 aggacagaggagccctccgggttgggttcttagcaggctccctgaagtccctagatgtgagcggcaaccctctg
caactgcgcctgtggggcagcccttggacttctgtgcaggttcaggctgcgtccgtctggctgcccagccgc
gtcaagtgtggcagtccggccagctccaggccgcagcatcttcgcacaagacactgcgcctctgcctggacaag
tccctctccctggactgtttggctctcattgtctgggttgcgtccctggccatgcctatgttgcaccac
ctctgcggctggacactctggactgtctccacactggccctggctggctgccccggcgggggtggcagcggggc
20 gccgatgcctcgagctatgtgccttggcttcgacaaggcacagagcgcagtgccgactgggttgcataat
gaactgcgggtgcggctagaggagcgcctggggccggcgtccgcctgtgtctggaggagcgtactggcta
cctggcaagacgcgttgcggccatgcggccctcagtcacagcagccgcagatgtctggctggccac
acggaccaggctcagtgcccttcgcgtccagcttcgtctggccccagcagcgcgtctgtggaggaccgcaggac
gttgtggctggtaatcctgagccctgacgcccgcgttcccggttacgtgcggctgcgcagcgcctctggcc
cagagtgcctcttctggcccccaccagccatgtggccagcgcagcttctggcccgacttaggcattggccctgacc
agggacaaccgcacttctataaccagaacttcgtccggggccgcacatggctgagtagcacaagactgacagcc
tggcatgtacaaccccccagccctgacccctgcctctgcctatgtgcctcactctgtgacccccc
tgctctgcctccgcaccctcaccctggcatacagcaggcactcaataatgcactggcaggccaaacagcca
aaaaaaaaaaaaaaaaaaaaaa

25

SEQ ID NO:16 (Equine TLR9)

- 17 -

cagggttcaggctgcgcgtgcctggctgcggccagccgcgtcaagtgtggcagtccggggccagctccaggggccgcagc
atcttcgcacaagacactgcgcctctgcctggacaagtccctctcttggactgttttggt

SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLLVQAAAALAAAALAQGTLPAFLPCELQPRGVNCNWLFLKSVPRFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLNSLRLVNLKWNCPAGLSPMHFFCRMTIEPNFTFLAVPTLEELNLSYNGITTVPALPSSLVSLSSL
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQAVEVAPGALLGLGNLTHLSLKYNLLEVPRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGVLKDSSLKLEK
DWFRLGLRQLVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFNYHKKVSPAHLQLAPSFGGLVSLKEKLDMHGIFF
10 RSLNTTLLRPLTQLPKLQSLSLQLNFINQAEELSIFGAFPSLLFVDSLSDNRISGAARPVAALGEVDSGVEVWRWPR
GLAPGPLAAVSAKDFMPSCNLFNTLDSLRSNNLVTIQQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD
LSYNKLDLYHGRSFTELPQLEALDLSSYNSQFMSMQGVGHNLSFVAQLPSLRLYLSLAHNGIHSRSVQSKLSSASLRA
LDFSGNSLSQMWAEGLYLCFFKGRLRNLVQLDLSKNHLHTLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP
QLEALDLAGNQLKALSNGLSPPGTRLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFWFGRLTETL
15 NIIDVSANPLHCAGAAFVDFLLEMQAAPGLSRRVTCGSPGQLQGRS1FAQDRLRLCDETSLSDCFGFSLMVA
LGLAVPMLHLCGWDLWYCFHLCLAHLPRRRRQRGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEERRGRRAL
RLCLERDWLPGKTLFENLWASVYSSRKTMFVLDDHTDRVSGLLRASFLAQQRLLEDRKDVVVLVILRPAAYRSR
YVRLQRLCRQSVLLWPHQPSGQGSFWANLGMALTRDNRHFYNRNFCRGPTTAE

20 SEQ ID NO:18 (Ovine TLR9)

25 MGPYCAPHPLSLLVQAAAALAAQGTLPAFLPCELQPRGKVCNCNWLFLKSVPRFSAGAPRANVTSLSLISNRIGHLHDSDFVHLSNLRLVNLKWNCPAGLSPMFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSSLRTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQADEVAPGALLGLGNLTHLSSLKYNLNLTEVPRLLPPSLDTLLLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPLKHPDTFSHLSRLEGVLKDSSLKLEKDWFRLGLRQLVLDLSENFLYDYITKTTIFRNLTQRLRLNLSFNYHKVSAFHQLAPSFGGLVSLKLDMHGIFFRSLTNTRLRLTOLPKLQSLSLQLNFINQAEELSFGAFPSLLFVDSLSDNRISGAARPVAALGEVDSGVEVWRWPRGLAPGPLAAVSAKDFMPSCNLNFTLDSLRSNNLVTIQQEMFTRLSRQLCRLSHNSISQAVNGSQFVPLTRLRVLDLSYNKLDLYHGRSFTELPQEALDLSSYNSQFMSQGVGHNLSFVAQLPSLRLYLSLAHNGIHSRVSQKLSSASLRA
30 LDFSGNSLSQMWAEGLYLCFFKGRLRNVLQDLSKHNHLHLLPRHLDNLPKSLRQLRLRDNNLIAFFNWSSLTVLPQLEALDLAGNQLKALSNGLSPPGTRLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFWFGRLTETLNJLDVSANPLHACGAAFVDFLLEMOAAVPGLSRRVTCGSPGOLOGRSIFAODLRLCLDETLSSLDCFG

SEQ ID NO:19 (Ovine TLR9)

35 gtccggcacgggaagtgagcgccaagcatccttcctgcagctgccgccaacttgcggccagaccctctggaga
agccgcattccctgccatgggcccactgtgccccgcaccccttctcttgcggtaaggtaactgcac
agcagccctggcccagggcaccctgcctgccttcctgcctgtgagcttgcagccccgggtaaggtaactgcac
ctggcttcttgcggtaactgtgccccgggagccccccgggcaatgtcaccagcttccttaat
cttcaaccgcacccaccacttgcacgactctgacttcgtccacccgtccaaacctgcgggtctcaaccccaactg
gaactgcccggccggccgtcagccccatgcacttccctgcggcatgaccatcgagccaaacacccttcctgg
40 tttgtgcccaccctggaggagactgaacctgagctacaatggcatcacgaccgtgcctggccagttctctgt
atccctgtcgctgagccgcaccagcatctggcttaggccccaccacttaccggcctgcacgcctcgctt
tctgtacatggacggcaactgtactataagaacccctgcacccggcgtggaggtggcccccaggccctct
tggcctgggcaacctcacgcacccgtcgctcaagtacaacaacctcacggaggtggcccccggctgccccccag
cctggacaccctgtgttccataaccacatcatcacccgtgcacccggaggaccctggccaatctgactggct
45 gctgtgtgttgcgtgtggggggactgcccggctgcgaccacccggcaaccctgcaggagtgccaaagaa
cttccccaactgtgcacccctgacacccctgacccctgcacccggctgcgaccacccggcaaccctgcaggagtgccaaagaa
ctacaaaactagagaaagactgggtcccgccctggcagggtccaactgtgtcgaccctgagtgagaacttcttca
tgactacatcaccaagaccaccatcttcaggaaacctgacccggactgcgacactcaacctgtccctcaattacca
caagaagggtgtccctcgcccacctgcaactggcaccccttggggcctgggttccctggagaagactggacat
50 gcaacggcatcttcttcgtccctcaccaacaccacgcgtccggccgtgacccagctgcccacacttccagact
gagtctgcagctgaacttcatcaaccaggccgagctcagcatcttggggcctcccgagccctgtcttgcgtgg
cctgtcgacaccgcacccgcacccggagctgcgaggccgggtggcccccctggggagggtggacagccgggtggaaag
ctggcggtggcccacggggctgcgtccaggccccgtggcccccgtcagcgcaaaaggacttcatgccaactgca

- 18 -

5 cctcaaccttacccgtggacctgtcacggaaacaacccgtgacgatccaggcaggagatgttacccgcctccccc
cctccagtgcctgcgcctgagccacaacagcatctcgccaggcggttaatggctcgccgtgaccgg
cctgcgagtgtcgaccctgtccataacaagctggacctgtaccatggcgctcgacggagctggcgacgt
ggaggcactggacccgtacaacagccagcccttcagcatgcagggcggtggccacaacccatcagcttcgtgg
ccagctgcgcgtccctgcgtacccctcagcgtgcacaacccgtatccacagccgcgtgtcacagaagctcagcag
cgccctcgctgcgcgcctggacttcagccgcaactccctgagccagatgtggcccgaggagacctctatctcg
cttcttcaaaaggcttgagggaaacctgggtccagctggacctgtccaaagaaccacccctgcacaccctcctgcctcgta
cctggataacccgtcccaagagccgtcgccgagctgcgtctccgggacaataacccgtccctctcaactggagcag
cctgactgttctgccccagctggaaacctggatctggcgaaaaccagctgaaggccctgagcaacccgcagcc
gccacccgtgcacccggctccagaagctggacgtgagccagcaacccgtatccgcgttgcaccctggcttgc
ccttgcacccggctgaaagagacttaacccctcagccaaacctggactggatccctctgggttggctcg
cttaacccggacttgcataatccctagccgtgagcccaacctccgtccactgtgcctgcggggcccttgc
cttccctgtggagatgcaggccgtgcctggctgtccaggccgtcacgtgtggcagtcggccagctcc
ggggccgcagcatcttcgcacaggacccgtccctgcctggatgagaccctctccctggactgttggottctc
15 gctgctaattgggtggcgctgggcctggcgccatgtgcaccacccctgtggctggacccgtggactgtt
ccacccgtgtctggccatttgcggccacggccggccggcagccggggcgaggacaccctgtctacatgccttcgt
ggtcttcgacaaggcgccaggactgcgtggccactgggttacaacccgtccgcgtgcagctggaggagccgg
cgccggccggggcgtccgcctgtccctggactgggtccctggcaagacccgtcttcgagaacctgt
ggcctcggttacagccgtaaagaccatgttcgtgtccgtgaccacccggacccgggtcagtgccctctgcgcgc
cagcttcgtgtccctggccacggccgttggaggaccgcagggatgtcggtgtcgatccctgcgcggcc
cgccctaccgggtcccgctacgtgcggctgcgcacccgcctgcgcggccagccgcgtccctctggcccccaccagcc
cagtggccagggttagctctggccaaacctggcatggccctgaccaggacaaccggccacttctataaccggaa
cttctgcggggggcccaacgcacccgtaaatgcacccgtactgcggcc

25 SEQ ID NO:20 (Ovine TLR9)

- 19 -

caggccggccgtgcctggctgtccaggcggtcacgtgtggcagtccggccagtcagccaggccgcacatcttc
gcacaggacctgcgcctctgcctggatgagacccttcctggactgcttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are
5 publicly available. For example, an amino acid sequence for canine TLR9 is available as
GenBank accession number BAC65192 and its corresponding nucleotide sequence is
available as GenBank accession number AB104899. An amino acid sequence for feline
TLR9 is available as GenBank accession number AAN15751 and its corresponding
nucleotide sequence is available as GenBank accession number AY137581.

10 Complete nucleotide and amino acid sequences for canine and feline TLR9 were also
determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on
comparison with known amino acid sequences of human and murine TLR9, it appears that
SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the
15 transmembrane domain, and at least a portion of the intracellular domain of canine TLR9
(See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively
extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide
sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides
91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-
20 822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on
comparison with known amino acid sequences of human and murine TLR9, it appears that
SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the
transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See
25 Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular
domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline
TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID
NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID
NO:25.

30

SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLVQAAALALALAGTLPALPCELQPHGLVNCNWFLKSVPRFSAAAPRGNVTSLSLYSNRI
HHLHDYDFVHFVHLRRLNLKWCPPASLSPMHFPCHMTIEPNTFLAVPTLEDLNLSYNSITTVPALPSSLVSLSL
SRTNILVLDPATLAGLYALRFLFLDGNCYYKNPCQQALQVAPGALLGLGNLTHLSLKYNLLTVVPRGLPPSLEYL

- 20 -

5 LLSYNHIITLAPEDILANLTALRVLVGGNCRRCDHARNPCRECPKGFPQLHPNTFGHLSHLEGIVLRDSSLYSLD
PRWFHGLGNLMLVLDLSENFLYDCITKTAKFYGLARLRRNLNSFNYHKVSAFHLLASSFGSLLSLQELDIHGIF
FRSLSKITLQSLAHLPMQLRLHLQLNFISQAQLSIFGAFPGLRYVDSLSDNRISGAAPEAAATGEVEADCGERVWP
QSRDLALGPLGTPGSEAFMPSCRTLNFTLDSLRSNNLVTVQPEMFVRLARLOCLGLSHNSISQAVNGSQFVPLSNL
RVLIDLSHNKLDDLYHGRSFTELPRLEALDLSYNSQPSMRGVGHNLFSVAQLPALRYSLAHNGIHSRVSQQLRSAS
SLRALDFSGNTLSQMWAEGDLYLRLFFQGLRSLVQLDLSQNRLHLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL
ALLPKLEALDLAGNQLKALSGNSLSPNGTQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL
AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGLPSRVKCGSPGQLQGRSIFAQDRLCLDEALSWVCFSSL
LAVALSLAVPMLHQLCGWDLWYCFHLCALWLPRGRRGVDALAYDAFFVFDKAQSSVADWVYNELRVQLEERRG
10 RRALRLCLEERDWWPGKTLFENLWASVYSSRKTLFVLARTDRVSGLLRASFLLAQRRLLEDRKDVVVLVILCPDA
HRSRYVRLRQLRCQSVLLWPHQPSGQRSFWAQLGTLTRDNRHFYNQNFCRGPTTA

SEQ ID NO:22 (Canine TLR9)

15 MGP CR GAL HP L S L L V Q A A L A L A L A Q G T L P A F L P C E L Q P H G L V N C N W L F L K S V P R F S A A A P R G N V T S L S L Y S N R I
H H L H D Y D F V H F V H L R R I N L K W N C P P A S L S P M H F C H M T I E P N T F L A V P T L E D L N L S Y N S I T T V P A L P S L L V S N R I
S R T N I L V L D P A T L A G L Y A L R F L F L D G N C Y Y K N P C Q Q A L Q V A P G A L L G L G N L T H L S L K Y N N L T V V P R G L P P S L E Y L
L L S Y N H I I T L A P E D L A N I T A L R V L D V G G N C R R C D H A R N P C R E C P K G F P Q L H P N T F G H L S H L E G I V L R D S S L Y S L D
P R W F H G L G N L M V L D L S E N F L Y D C I T K T K A F Y G L A R L R R L N L S F P N Y H K V S F A H L H L A S S F G S L L S L Q E L D I H G I F
F R S L S K I T T L Q S L A H L P M L Q R L H L Q L N F I S Q A Q L S I F G A F P G L R X V D L S D N R I S G A A E P A A A T G E V E A D C G E R V W P
20 Q S R D L A L G P L G T P G S E A F M P S C R T L N F T L D L S R N N L V T V Q P E M F V R L A R L Q C L G L S H N S I S Q A V N G S Q F V P L S N L
R V L D L S H N K L D L Y H G R S F T E L P R L E A L D L S Y N S Q P F S M R G V G H N L S F V A Q L P A L R Y L S L A H N G I H S R V S Q Q L R S A
S L R A L D F S G N T L S Q M W A E G D L Y L R R F F Q G L R S L V Q L D L S Q N R L H T L L P R N L D N L P K S L R L L R L R D N Y L A F F N W S S L
A L L P K L E A L D L A G N Q L K A L S N G S L P M G T Q L Q R L D L S G N S I G F V V P S F F A L A V R L R E L N L S A N A L K T V E P S W F G S L
A G A L K V L D V T A N P L H C A C G A T F V D F I L L E V Q A A V P G L P S R V K C G S P G Q L O G R S I F A Q D L R L C L D E A L S W V C F S

SEQ ID NO:23 (Canine TLR9)

30 aggaaggggctgtgagctccaaggcatccttcctgcagctgtgcggccagccgcggccagaccctctggagaag
cccccgctccctgtcatgggccccctgcgcgtggccctgcaccccccgtctctcctggcggactgcctggcgtca
gcctggccctggcccagggcacccctgcctgcctgcctgtgagctccagcccatggcgttggtaactgc
aactggctgtccctcaagtccgtgcggccgttctcgccagctgcaccccggttaacgtcaccaggcttccttg
tactccaaccgcacccacccatccatgactatgactttgtccacttcgtccacctgcggcgtcaatctcaag
tggaaactgcccggccgcaggcctcagccccatgcacttgcctgtcacatgaccattgagcccaacaccccttcctg
gctgtgcccaccctagagggacctgaatctgagctataacagcatcacgactgtgcggccctgcggcgttgcctt
gtgtccctgtccctgagccgcaccaacatcctgtgtgcggccctgcacccctggcaggccttatgcctgc
35 ttccctgttcctggatggcaactgctactacaagaacccctgcagcagggccctgcaggtggcccccagggtccct
ctggggcctggcaacctcacacacccctgtcactcaagtacaacaacccatcaccgtggccgcggggcctgc
agccctggaggtaacctgtcttgcctacaaccacatcatcacccctggcaccctgaggacactggccaaatctgactgg
ctgcgtgtccctcgatgtgggtggaaactgtgcgcgtgtgaccatgcctgtgaggagtgccca
ggcttcccccaagctgcaccccaacacccctggccacctgagccacccctgagaaggcctgtgtgaggagacgctt
40 ctctacagccctggaccccagggtggttccatggcctggcaacccatggtgtgcgcactgagaacttccct
tatgactgcatcacaaaaccaagcccttacccctggccggctgcgcagactcaacccatgc
cataagaagggtgtccttgcacccatgcacccatgcaccccttgcggagccactgtccctgcaggagctgg
atacatggcatcttcttcgcctgcctcagcaagaccacgcgtccagtcgtgcggccacccatgc
45 ctgcacatgcactgtgaaactttatcagccaggcccagctcagcatcttcggcccttccctggactgcggtaactgt
gacttgtcagacaaccgcacatcagtgaggctgcagagcccgccgtccacaggggaggtagaggcagactgtgg
gagagagtctggccacagtcccgggacccctgtctggggccacttggccacaggggaggtagaggcagactgtgg
agctgcaggaccctcaacttcacccctggacccctgtctggaaacaacccatgtactgtc
50 cggctggcgcgcctccagtgccctggccgtgaggccacaacagcatctcgccaggccgtcaatggctcg
cctctgagcaacccctgggggtgtggacccctgtccatcataacaagctggacccctgtaccacggcc
ctgcccgggtggaggccctggacccctcagcatacaacagccaggcccttcagcatgc
agctttgtggcacagctggcagccctgcgtacccctcagccctggcgcacaatggcatcc
55 cagctccgcagcgcctcgccctggggccctggacttcagtgccaaatccctgagcc
cttatctccgttcttcaaggccctgagaaggcctgtaccacggcc
ctgcccacgcacccctggacaacccctcccaagagccctgcggcc
aactggagcagccctggcccttccatccaaagctgg
aagccctggacccctggccggaaaaccaggctgaaggccctgagc

- 21 -

SEQ ID NO:24 (Canine TLR9)

SEQ ID NO:25 (Feline TLR9)

55 MGPCHGALHPPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDFLFLKSVPHFSAAAPRGNVTSLSLYSNR
HHLHDSDFVHLSSLRRLNLKWNCPPASLSPMHPFCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLVLSLS

- 22 -

5 SRTNILVLDPANLAGLHSLRFLFLDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNLAVPRLPPLSLEYLL
LLSYNHIITLAPEDLANLTALRVLVDVGGNCRRCDHARNPCMCECPKGFPHLHPDTSFSLNHLLEGVLKDSSLN
PRWFHALGNLMVLDSNENFLYDCITKTTAFQGLAQLRLNLSFNYHKKVSAHLHLAPSFGSLLSLQQLDMHGIF
FRSLSETTLRSLVHLPMLQSLHLMQMFINQAQLSIFGAFPGLRYVDLSNDRISGAMELAAATGEVDGGERVRLPS
GDLALGPPGTPSSEGFMPCGKTLNFTLDLSRNNLVTIOPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV
LDLSHNKLDLYHGRSFTELPRLAEALDLSYNSQPFMSMQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL
RALDFSGNALSRMWAEGDLYLHFFRGLRSVLVRLDLSQNRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSLVL
LPRLEALDLAGNQLKALSNGSLPNTGQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG
10 TLKVLDVTGNPLHACGAAFVDFLLEVQAAVPGLPGHVKGSPGQLQGRSIFAQDLRLCLDEALSWDCFGSLLT
VALGLAVPMLHHLCGWDLWYCFHCLAWLPRRGRRGADALPYDAFVVFDAQSAVADWVYNELRVLEERRGR
ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQLLEDRKDVVVLVILRPDAHR
SRYVRLQRQLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFCRGPTTAE

SEQ ID NO:26 (Feline TLR9)

15 MGPCHGALHPLSLVQAAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLYSNRI
HHLHDSDFVHLSSLRRLNLKWNCPPASLSPMHFPCHMTIEPHTFLAVPTLEELNSYNSTITVPALPSSLVSLSL
SRTNILVLDPANLAGLHSLRFLFLDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNLAVPRLPPLSLEYLL
LLSYNHIITLAPEDLANLTALRVLVDVGGNCRRCDHARNPCMCECPKGFPHLHPDTSFSLNHLLEGVLKDSSLN
PRWFHALGNLMVLDSNENFLYDCITKTTAFQGLAQLRLNLSFNYHKKVSAHLHLAPSFGSLLSLQQLDMHGIF
20 FRSLSETTLRSLVHLPMLQSLHLMQMFINQAQLSIFGAFPGLRYVDLSNDRISGAMELAAATGEVDGGERVRLPS
GDLALGPPGTPSSEGFMPCGKTLNFTLDLSRNNLVTIOPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV
LDLSHNKLDLYHGRSFTELPRLAEALDLSYNSQPFMSMQGVGHNLFSVAQLPALRYLSLAHNDIHSRVSQQLCSASL
RALDFSGNALSRMWAEGDLYLHFFRGLRSVLVRLDLSQNRLHTLLPRTLDNLPKSLRLLRLRDNYLAFFNWSSLVL
LPRLEALDLAGNQLKALSNGSLPNTGQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG
25 TLKVLDVTGNPLHACGAAFVDFLLEVQAAVPGLPGHVKGSPGQLQGRSIFAQDLRLCLDEALSWDCFG

SEQ ID NO:27 (Feline TLR9)

30 agggtgtcgcagtcaggcattttctgcattgcgtgcgcactgtgcacccctctggagaagcccc
cactccctgtcatggggccctgcattggccctgcacccctgtctcttcgtgcaggctgcgcgtggcc
tggccctggcccaaggccacccctgcattttctgcgcggcagccccctgtgtacgcgcacggcctgg
ggctgttcctcaagtccgtgcgcacttctcgccggcagccccctgtgtacgcgcacccctgtact
ccaacccgcacccatccacgcactccgcactttgtccacccctgtccagccgcgcgttcacac
actgcccacccgc
tgc
35 ccctgtccttgaggcgtgaaccttgactacaacacgcacccatccgcgcgcgcgcgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgcgcgcgcgc
tgc
ccctgtccttgaggcgtgaaccttgactacaacacgcacccatccgcgcgcgcgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgcgcgcgc
40 tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgcgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
45 acctgcacatgcacccatccgcgcgcgcgcgcgcgcgcgcgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
50 tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc
55 tggccacccctggaggcgtgaaccttgactacaacacgcacccatccgcgcgc

- 23 -

5 gcctggccctccccaggctggaaaggccctggacactggcggaaaccagctgaaggccctgagcaacggcagct
tgcctaatggaaaccagctccagaggctggacctcagcagcaacagtatcagcttcgtggccctccagcttttttg
ctctggccaccaggctgcgagagctcaacctcagtgccaaaggccctcaagacggtgagccctcctggttcggtt
ctctagcgggaccctgaaaagtccctagatgtgactggcaacccctgactgcgcctgtggggcccttcgtgg
acttcttgcggaggtgcaggctgcagtgcccccgcctgcccaggccacgtcaagtgtggcagttccaggtcagctc
aggccgcagcatcttgcgcaggatctgcgcctctgcctggatgaggccctctctggactgtttggccct
cgctgcgtgaccgtggccctgggcctggccgtgcccattgcgcaccacctctgtggctggactctgttactgt
tccacactgtgcctggccctggctgccccggcgggggcgccggcgccggatgcctgcctacgtgccttgg
tggtcttcgacaaggcacagagcgcggtgccactgggttgcacaacgcgtgcgggtacggctagaggagcc
gtggacgcgcagcgtccgcctgtgcctggaggaacgtgactggctacccggtaaaacgcgtctttgagaacctgt
ggccctcagttacagcagccgcagatgctgtttgtgcctggccacacagacagggtcagccgccttgcgc
ccagcttcgtggcccgccagcagcgcctgtgcggaggaccgcagggacgttgcgttgcgttgcgc
acgcccacccgcctccgcgtatgtgcggctgcgcagcgcctgtgcgcacagggacgcgtcctctggcccccaccagc
ccagtgcccgccagcgcagttctggcccgccagctgggcacggccctgaccaggacaaccagcacttctataaccaga
acttctgcggggcccccacgcacggcagactgaccgcctgcaccccaagcctcctacacccttcgtctgcctg
ggatgcgggg

SEQ ID NO:28 (Feline TLR9)

20 atggggccccctgcacatgggcgcctgcaccccccgtctctccctgggtcagggctgcgcgcgtggccgtggccctggc
caggggcacccctgcctgccttctgcctgtgagctccagcgcacggcgtggtaattgcactggctgtttctc
aagtccgtgccccacttctcgccggcagcgcggccgtggtaacgtcaccaggcttcctgtactccaaccgcac
caccacccacactccgactccgactttgtccacctgtccagcgcctggcgtctcaacctaaatggaaactggccac
gccagcctcagccccatgcacttccctgtcactatgaccattgagccccacaccttctggccgtggccacccctg
gaggagctgaacctgagactacaacagcatcagcagacttccctggccctggccagttccctgtgtccctgtcttg
25 agccgtaccaacatcctgggtctgggaccctgcaacccctcgccaggcgtgcactccctgcgtttctgttccctggat
ggcaactgtactacaagaacccctgcccgcaggccctgcagggtggcccccggcccttctggctggcaac
cttacgcacctgtcactcaactacaacacactcgccgtccccccggccctgccccccagctggagttacctg
ctattgtcctacaaccacatcatcaccctggccctgaggacctggccaaacctgaccggccctgcgtgtgtctgat
gtgggtggaaactggcgtcgctgtgaccacgcccccaacccctgtatggagtggcccaagggtctccgcacctg
30 caccctgacacccctcagccacccctgaaaccacccctcgcaaggcgtgttgaaggacagctctctacaacctgaa
cccagatggttccatgcctggcaacccctatgggtctggacactgagtgagaacttcttatatgactgcac
aaaaccacagcccccaggccctggcccaactgcgcagactcaacttgccttcaattaccacaagaagggtgtcc
tttgcacccctgcacatctggccccccttcgggagccctgcctccctgcagcagctggacatgcacatggcatctt
ttccgctcgtcagcgagaccacgctccggcgtctggccacccctgcctccagactgcacctgcagatg
35 aacttcatcaatcaggcccagctcagcatcttcggggccttcctggcgtgcatacgtggacctgtcagacaac
cgataagtggagccatggagctggggctgccccccgg
ggggacctagctctgggcccacccggccacccctagctccgagggcttcatgcctggcggcgtcaagaccctcaactt
acccctggacctgtcacggaaacaaccttagtgcacaatccagccagagatgtttggccggctctcgccgcctccagtg
40 ctgctccctgagccgcaacagcatctcgccaggcgtcaacggctcacaatttatggcgtgaccaggctgcaggtg
ctggacctgtcccataacaagactggacactgttaccatggcgtctttcagggagctggcggcgtggaggccctg
gacctcagctacaacagccagccgcacccctcagcatgcagggcgtgggtcacaacccctcagcttgcacagctgc
gcctgcgtatctcagcctggcgcacaacgcacatccacagccgtgttcccagcagctctgcagcgcctcgctg
cgcccttggaacttcagccgcaatgccttgcgggatgtggccggagggagccctgtatctccacttctccga
45 ggccctgaggagccctggcgtccgggtggatctgttcccagaatgcctgcatacccttgcacgcaccctggacaac
ctcccccaagagccctgcggcgtctgcgttccgtgacaattatctggcttcttcaactggagcagccctggctctc
ctccccccaggctggaaagccctggacccctggggaaaccagctgaaaggccctgagcaacccggcagctgccttaatgg
acccagctccagaggctggacccctcagcagcaacagttatcagcttgcgtggccctccagcttttgcctggccacc
aggctgcgagagactcaacctcagtgccaaacgcctcaagacgggtggagcccttctgggttgcgttcttagccggc
50 accctgaaagtccctagatgtactggcaacccctgcactgcgcctgtggggccggcctcgtggacttctgtg
gaggtgcaggctgcagtgcggccctgcaggccacgtcaagtgtggcagttccaggctcagctccaggccgcage
atctttgcgcaggatctgcgccttgcctggatgaggcccttctggactgtttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

SEQ ID NO:29 (Murine TLR9)

15 MVLRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAACSNITRLSLISNRI
HHLNNSDFVHLSNLRQLNLKWCNCPPGLSPLHFSCHMTIEPRTFLAMRTLEELNSYNGITTVPRLPSSLVNLSSL
SHTNILVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGVLVKDSSLHTLN
SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLFSFNYRKKVSVARLHLASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHQMFNINQAQLSIFGTFRALRFVDSLSDNRISGPSTLSEATPEEADDAEQEELL
20 SADPHPAPLSTPASKNFMDRCKNFKFTMDLSRNNLVITKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSMKGIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLSNS
VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLDNLPKSLKLLSLRDNYLSFFNWTSL
FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNIKTVDRSWFGPIV
MNLTVIDVRSNPLHCACGAAFDV DLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGSL
25 25 AVAVGMVVPILHLCGWDVWYCFHCLAWLPLLARSRRSAQALPYDAFVVFDKAQSAVADWVYNELRVLEERRG
RRALRLCLEDRDWLPGQTLFENLWASIYGRKTLFVLAHTDRVSGLLRTSFLAQQRLLLEDRKDVVVLVILRPDA
HRSRYVRLRQRLCRQSVLFWPQQPNGQGGFWAQLSTALTRDNRHFYNQNFCRGPTAE

SEQ ID NO:30 (Murine TLR9)

30 MVLRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAACSNITRLSLISNRI
HHLNNSDFVHLSNLRQLNLKWCNCPPGLSPLHFSCHMTIEPRTFLAMRTLEELNSYNGITTVPRLPSSLVNLSSL
SHTNILVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYL
LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIIECGQKSLHLHPETFHHLSHLEGVLVKDSSLHTLN
SSWFQGLVNLSVLDLSENFLYESINHTNAFQNLTRLRKLNLFSFNYRKKVSVARLHLASSFKNLVSLQELNMNGIF
FRSLNKYTLRWLADLPKLHTLHQMFNINQAQLSIFGTFRALRFVDSLSDNRISGPSTLSEATPEEADDAEQEELL
35 SADPHPAPLSTPASKNFMDRCKNFKFTMDLSRNNLVITKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSMKGIGHNFSFVAHLSMLHSLSLAHNDIHTRVSSHLSNS
VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLDNLPKSLKLLSLRDNYLSFFNWTSL
FLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNIKTVDRSWFGPIV
40 MNLTVIDVRSNPLHCACGAAFDV DLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

SEQ ID NO:31 (Murine TLR9)

tgtcagagggagccctgggagaatcctccatctcccaacatggttctccgtcgaaggactctgcaccccttgtcc
ctcctggtagggctgcagtgctggctgagactctggccctgggtaccctgccttcctaccctgtgagctg

- 25 -

SEQ ID NO:31 (Murine TLR9)

45 atggttctccgtcgaggactctgcaccccttgcctgtccctcctggatcaggctgcagtgcgtggctgagactctggc
 ctgggtaccctgcctgccttccatccctgtgagctgaagctcatggcctggactgcataattggctgttctgt
 aagtctgtaccccgtttctgcggcagcatctgtccaaatcaccgcctctcctgtatctccaaccgtatc
 caccacctgcacaactccgacttcgtccacctgtccaaacctgcggcagctgaacctcaagtggactgtccacc
 actggccttagccccctgcacttcttgcacatgaccatigagccagaaccttctggctatgcgtacactg
 50 gaggagctgaacctgagctataatggtatcaccactgtgccccgactgcccagctccctggtaatctgagcctg
 agccacaccaaacatcctggttctagatgctaacagcctgcggcctatacagcctgcgcgttotcttcatggac
 gggactgctactacaagaacccctgcacaggagcggtaaggtgaccccaaggcgcctctggcctgagacaat
 ctcacccatctgtctctgaagtataacaacctcacaagggtccccgccaactgccccccagctggagtagactc
 ctggtgtcctataacctcattgtcaagctggggctgaagacctggccaatctgaccccttcgtactttagt
 55 gtgggtggattgcgcgtcgctgacccatgcctgtatagaatgtggaaaagtcctccacctg
 caccctgagacccatcacctgagccatctggagggcctgtgtgaaggacagctctccatcacactgaac
 tcttcctgggtccaaggctggtaacccctcggtgtggacctaagcgagaacttctctatgaaagcatcaac
 cacaccaatgccttcagaacctaaccgcctgcgcagctcaacctgtcctcaattaccqcaaaagctatcc

- 26 -

5 tttggccgcctccacctggcaagttcctcaagaacctgggtcactgcaggagctgaacatgaacggcatcttc
 ttccgcgcgtcaacaagtaacacgcgtcagatggctggccgatctgcccactccacactctgcacatctcaaatg
 aacttcatcaaccaggcacagtcagcatcttggtaacctccgagccctcgcttggacttgcagacaat
 cgcatcagtgggcctcaacgcgtcagaagccaccctgaagaggcagatgcagagcaggaggagctgttg
 tctgcggatcctcaccagctccactgagcaccctgcctcaagaacttcatggacagtgtaagaacttcaag
 ttcaccatggaccctgtctcgaaacaacctggtaactatcaagccagagatgttgcataatctctcacgcctccag
 tgccttagcctgagccacaactccattgcacaggctgtcaatggctctcaggcctgactaatctgcag
 gtgcggaccctgtcccataacaaactggacttgcactggaaatcggtcagtgcagttaccacagttgcaggcc
 ctggacactgagctacaacagccagcccttagcatgaaggataggccacaatttcagggttgcggccatctg
 10 tccatgctacacagccttagcctggcacacaatgacattcataccctgtgcctcacatctcaacagcaactca
 gtgagggttctgacttcagccgcaacggtatggccgcgttgcataatctccgcggccagaacccctgac
 caaggcctgagtggcctgtgaagctggaccctgtctcaaaaataacctgcataatctccgcggccagaacccctgac
 aaccccccagagcctgaagctgcgtgagccgcgagacaactacctatcttcattactggaccagtcgtcc
 15 ttcctgcccacactggaaacttgcacttagcctggcaggcaaccagctaaaggccctgaccaatggcaccctgcataat
 ggcaccctcctccagaaactggatgtcagcagcaacagttatcgctctgtgtgcctcgcctctggc
 gtcgagctgaaagaggtaacccctagccacaacatttcagacgggtatcgctctgtgttggccatctgt
 atgaacctgacattctagacgtgagaagcaacccctgcactgtgcctgtggcagccctgttagacttactg
 ttggaggtgcagaccaaggtgcctggcttaatgggtgtgaagtgtggcagcccccggcagctgcaggccgt
 20 agcatcttcgcacaggacctgcggctgtgcctggatggcttcatttggactgtttggc
 SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPFSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPRLRHLNLKWNCPPVGLSPMHPCHTIEPSTFLAVPTLEELNLSYNNIIMTVPALPKSLISLSL
 25 SHTNILMldsASLAGLHALRFLFMDGNYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL
 LLSYNRIVKLAPEDLANLTALRVLVDVGGNCRRCDHAPNPMCECPHFPQLHPDFTFSHLSRLEGLVLDSSLSWLN
 ASWFRGLGNLRLVLDLSENFLYKCITKTFQGLTQLRKLNLSPFNYQKRVSAHLSLAPSFGSLVALKEELDMHGIF
 FRSLEDETTLRPLARLPMQLTQLRQLQMFNINQAGLGIIFRAFPGLRYVLDLSDNRISGASELTATMGEADGGEKVWLQP
 GDLAPAPVDTPSSEDPRPNCASTLNFTLDLISRNLLTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 30 LDLSRNKLDLYHEHSTELPREALDLISYNSQPFGMQGVGHNFVFVAHLRTLRLSLAHNNIHSQVSQLCSTS
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVRLRDNLYLAFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS
 ALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAFQDLRLCLDEALSWDCFALSLLA
 35 VALGLGVPMHLHLCGWDLWYCFHLCALWLPWRGRQSGRDEDALPYDAFVVFDTQSAVADWVYNELRGQLEECRG
 RWALRLCIEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLAQQRLLLEDRKDVVVLVILSPDG
 RRSRYVRLQRQLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAE

SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPFSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPRLRHLNLKWNCPPVGLSPMHPCHTIEPSTFLAVPTLEELNLSYNNIIMTVPALPKSLISLSL
 40 SHTNILMldsASLAGLHALRFLFMDGNYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL
 LLSYNRIVKLAPEDLANLTALRVLVDVGGNCRRCDHAPNPMCECPHFPQLHPDFTFSHLSRLEGLVLDSSLSWLN
 ASWFRGLGNLRLVLDLSENFLYKCITKTFQGLTQLRKLNLSPFNYQKRVSAHLSLAPSFGSLVALKEELDMHGIF
 FRSLEDETTLRPLARLPMQLTQLRQLQMFNINQAGLGIIFRAFPGLRYVLDLSDNRISGASELTATMGEADGGEKVWLQP
 GDLAPAPVDTPSSEDPRPNCASTLNFTLDLISRNLLTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 45 LDLSRNKLDLYHEHSTELPREALDLISYNSQPFGMQGVGHNFVFVAHLRTLRLSLAHNNIHSQVSQLCSTS
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVRLRDNLYLAFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLAS
 ALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAFQDLRLCLDEALSWDCFA

50 SEQ ID NO:35 (Human TLR9)

aggctggtataaaatcttacttccttattctctgagccgtctgtccctgtggaaaggacctcgagtgtga
 agcatcttcctgttagctgtccagtcgtccggccagaccctctggagaagccctgtcccccacatgggt
 ttctgcggcagccgcctgcaccctgtgtctctctgtgcaggccatcatgtgtccatgaccctggccatgggt

- 27 -

5 accttgcctgccttctaccctgtgagctccagccccacggcctggtaactgcacactggctgttcctgaagtt
gtgccccacttccatggcagcacccctggcaatgtcaccagccttcctgtctccaaccgcacccaccac
ctccatgattctgactttgcccacctggccagcctggcatctcaacctcaagtggaaactgcccgggttggc
ctcagccccatgacttccctgccccatgaccatcgagcccagcacccatggctgtgcccaccctggaaagag
ctaaacctgagctacaacaacatcatgactgtgcctgcgtgccccatccctcatatccctgtccctcagccat
accaacatccatggctgactctgcagcctcggccctgcattgcctgcgttccattatggacggcaac
tggattacaagaacccctgcaggcaggcactggaggtggccctcctggctggcggcaacccatcacc
cacctgtcactcaagtacaacaacccatgtgtgcccccaacccatggctccagcctggagatctgtgtt
tcctacaaccgcacatgtccaaactggcgcctgaggacccatctgaccgcctgcgtgtcgtatgtggc
gaaaattgcccgcgtgcgaccacgcctccaaacccctgcattggagtgccctgcacttcccccagctacatccc
gataccttcagccacccatggccgttgcaggcctgttgcaggacagttctctctggcgtgaatggcagg
tggttccgtggctggaaacccctggcaggcactggacccatggcgtgagaacttctctacaaatgcacactaaaacc
aaggcctccaggcctaaacacagctgcgcaagcttacccatggctccattaccaaaagagggtgtcccttgc
cacctgtctctggcccttcctggcggagccctgtcggccctgaaaggagctggacatgcacggcatcttctccgc
15 tcactcgatgagaccacgcctccggccactggccgcctgcccattgcctcagactctgcgtctgcagatgaactt
atcaaccaggcccacgcctggcatctcaggccctccctggcctgcgtacgtggacccatgtcggacaaccgcac
agcggagcttcggagactgcacagccacccatggggaggcagatggagggagaaggctggctgcagccctgggac
cttgcctccggcccccagttggacactccagcttcgaagacttccaggccaaactgcacgcaccctcaacttccat
gatctgtcaccggaaacaacccatggtaccgtgcaggccggagatgttgcctccagcttcgcacccatgcagtgcc
20 ctgagccacaactgcacccatgcaggcactgcataatggctccctggcgttgcacccgtctgcagggtctagac
ctgtcccgcaataagctggacccatccacgcacccatgcattcaggcactaccgcactggagggccctggaccc
actacaacacagccacccatggcatgcaggcgtggccacaacttcagttcgtggctcacctgcacccat
ccggccacccatgcggccacaacacatccacgcacccatgcaggcgtggccacccatgcacccat
ctggacttcagccggcaatgcactggccatatgtggccggagacccatgcacttccatgcacttccaaaggcctg
25 agcggtttgcgtggacttgcctccagaaccgcctgcacccctctggccaaaccctgcgcacccat
aagagcctacaggcgtgcgtccctggcatgcacccatggccacaacttcagttcgtggctcacccat
aaacttggaaacttcctcgacccatggcaggaaaccggcgtgaaggccctgaccaatggcaggcctgcctgtggc
ctccggaggcgtggatgtcagctgcacccatgcacccatgcacccatgcacccat
cgagagctcaacccatgcggcaacccctcaagacccatgcacccatgcacccat
30 caaataacttagatgtaaaggcacaacccctgcactgcgcctgtggccgccttattggacttccctgtggagg
caggcgtccgtggccggctgcctggccacccgggtgaagtggtggcactccggccagccctgcacccat
gcacaggacccatgcgcctgcctggatggccctctggactgttgcctccatgcacccat
ctggccctgggtgtgcccattgcacccatgcacccatgcacccat
tggcttccctgg
35 aaaacgcagagcgcagactggcagactgggttgcacccatgcacccatgcacccatgcacccat
gcactccgcctgtgcctggaggaaacccgcactggcgtgcctggcaaaacccttgcacccat
tatggcagcccaagacgcgtttgtgcgtggccacacggaccgggtcaagtggtcttgcgcgcacccat
ctggccctggcggccatgcacccatgcacccatgcacccat
tcccgcacgtgcggcgtgcggccacccatgcacccatgcacccat
40 cgccagcttctggcccaacggcatggccctgaccaggacaaccaccatccatataaccggaaacttctggc
ggacccacggccgaatagccgtgaggccgaatctgcacccgtgcacccatccacactcaccctcacc
tggctgaccctccctgcgtccctccatccacccatgcacccatgcacccat

SEQ ID NO:36 (Human TLR9)

45 atgggtttctgcgcagccccctgcacccgtctctccctggcagggccatcatgtggccatgaccctggc
ctgggtacctgcctgccttccatccctgtgagctccagccccacggcgttgaaactgcacactggctgttctg
aagtctgtgccccacttctccatggcagcaccggcgttgcaatgtcaccaggccttcttgccctcaaccgcac
caccacccatgattctgactttggccacctggccagcgttgcggcatctcaacctaagtggaaactggccggc
gttggcctcagccccatgcacttccctgccacatgaccatcgagccccagcaccttcttgctgtggccaccc
gaagagctaaacctgagactacaacaacatcatgactgtgcctgcgtggccaaatccctcatatccctgtccct
50 agccataccacccatctgtatgactctgcacccgtcgccggcgttgcatgcctgcgttcttattcatggac
ggcaactgttattacaagaaccctgcaggcaggcactggaggtggccgggtgccttcattggctggcaac
ctcaccacccatgtcactcaagtacaacaacactcaactgtggccggcaacctgccttcagctggagttatctg
ctgttgcctacaaccgcacgtcaactggcgcctgaggacactggcaatctgaccggccctgcgtgtgcctgat
55 gtggggcgaaattggccggcgtgcgaccacgcgtcccaaccctgtcatggagtgccctgcgtacttccca
catcccgatcacccatggccacctgagccgttgcaggcgttgaaaggacacttgcctctggctgaat
gcccggatgggttccgtggctggaaacctccgagtgctggacactggatgtgagaacttccatcacaaatgcac
acttccatcacacttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgtt

5 aaaaccaaggccttcaggcccataacacagctgcgaagcttaacctgtccttcaattacccaaaagagggtgtcc
ttgcccacctgtctggccccttcctcgggagcgtggtcgcctgaaggagctggacatgcacggcatcttc
ttccgctactcgatgagacaccacgcgtccggccactggccctgcctgcctgcccacactgtcgctgcagatg
aacttcatcaaccaggcccagctcgcatcttcaggccttcctggcctgcctacgtggacctgtcgacaaac
cgcatcagcggagcttcggagctgacagccaccatggggaggcagatggagggagaagggtcggtgcagcct
ggggaccttgcgtccggcccccagtggacactcccagctgtgaagacttcaggccaaactgcagcaccccaacttc
accttggatctgtcacaaggaaacaacctggtgaccgtgcagccggagatgttgcctcagcttcgcacactgcagtgc
ctgcgcctgagccacaactgcacactcgccaggcagtcaatggctccagttctgcgcctgaccggctgcaggtg
ctagacctgtcccgcaataagctggaccttaccacagcacttacacggacttacccgcactggaggccctg
10 gacctcagctacaacacagccaggcccttgcacatgcaggcgtggccacaacttcagcttcgtggctcacctgcgc
accctgcgcacccatcagcgcctggccacaacaacatccacagccaaagtgtcccgacgcgcacttcgcacgtgc
cgccctggacttcagccgaatgcacttggccatatgtggggcaggagacctctatctgcacttcttccaa
ggcctgagcggtttgcgttgcacttgccttgcacacccttcgcgccttgcgccttgcgcac
ctccccaagagccatcaggtgcgttcgtgacaattacctggcttcgttgcgccttgcgcacttgc
15 ctgcccaaactggaaagtgcctcgacctggcaggaaacccggctgaaggccctgaccaatggcagccgcgc
acccggctccggaggcgtggatgtcagctcaacagcatcagcttcgtggcccccggcttctttccaaaggccaaag
gagctgcagagactcaaccttagcgcacgcctcaagacagactggaccacttcgtggcccttgcgc
gcctgcacacttagatgtaaagcgcaccccttcgcacttcgcgcctgtggccgccttatggacttcctgc
gaggtgcaggcgtccgtgcgggtctgcctcggcgggtgaagtgtggcagttccggccagctccaggccctc
20 atcttgcacaggacactgcgccttcgcctggatgaggcccttcgcgccttgcgc
atcttgcacaggacactgcgccttcgcctggatgaggcccttcgcgccttgcgc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9
25 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and
nucleic acid molecules encoding them are provided by the invention. The chimeric
polypeptides include at least one amino acid substitution based on a comparison of
conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,
equine, ovine, canine, feline, and human TLR9. The information contained in a multiple
sequence alignment of these various TLR9 polypeptide sequences, provided for example in
Figure 1, can be used to identify and select individual amino acid positions and even
30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or
substitutions can be effected using methods known to those of ordinary skill in molecular
biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be
inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino
35 acid for a second amino acid, wherein side chains of the first amino acid and the second
amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to
alter conformation. For example, conservative amino acid substitutions generally may be
made between members within each of the following groups: hydrophobic (A, I, L, M, V),
neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-
40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase, β -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art. The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be "operably linked" when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be "operably linked" when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A "TLR9 ligand" as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

5 The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

10 A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

15 In one embodiment a CpG nucleic acid is represented by at least the formula:



wherein X_1 and X_2 are nucleotides, N is any nucleotide, and N_1 and N_2 are nucleic acid sequences composed of from about 0-25 N 's each. In some embodiments X_1 is adenine, guanine, or thymine and/or X_2 is cytosine, adenine, or thymine. In other embodiments X_1 is cytosine and/or X_2 is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a 25 non-sequence specific manner.

30 An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

- 33 -

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, 10 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

15 For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the β -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); 20 Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 25 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease). 30 Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has
5 been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.
10 Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by
15 reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs,
20 such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

25 Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid
30 phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000) 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCM E C	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCM I C	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5	hTLR9 Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
	mTLR9 Q-VLDLSHN-K-L-D-L-Y-HWKSFSELP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

15 An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or 20 lipopolysaccharide, a small molecule.

25 A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including κB kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF-κB. Examples of such promoters include, without limitation, those for NF-κB, IL-1 β , IL-6, IL-8, IL-12 p40, CD80, CD86, and TNF- α . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase, β -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- α). In certain embodiments the reporter is selected from IL-8, TNF- α , NF-κB-luciferase (NF-κB-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

- 38 -

Mol Cell Biol 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982).

At least one of these reporter constructs (NF- κ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, 5 color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

10 According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of 15 quantitative measurements of responses in each instance.

In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a 20 TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of 25 a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I κ B, NF- κ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for 30 screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

Cells and Tissues. Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in *RNAlater*™ (Ambion®, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

First-strand cDNA synthesis. Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzolTM reagent (GIBCO BRL[®], Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using 5 SUPERSCRIPTTM II reverse transcriptase (GIBCO BRL[®], Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T₍₁₈₎]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at 10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl₂) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERSCRIPTTM II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:
20 forward primer 5'-ACCTTGCCTGCCTTCCTACCCGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38). The 2.7 Kbp fragment was PCR amplified using Advantage[®] 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix 25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

30 *Cloning and sequencing.* The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZErOTM - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment 5 were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

10 Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

15 *Results.* Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

20 Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, www.cmbi.kun.nl/bioinf/tools/clustalw.shtml). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple 25 sequence alignment are presented in **Figure 1**. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino 30 acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, 5 horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s 10 in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clonetech) were individually cloned into the expression vector 15 pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

20 Since NF- κ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- κ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- κ B-luciferase reporter plasmid (NF- κ B-luc) or with hTLR9 alone. 25 After stimulus with CpG-ODN (2006, 2 μ M, TCGTCGTTTGTGCGTTTGTGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 μ M, TGCTGCTTTGTGCTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

30 Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- κ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 μ M; TCCATGACGTTCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 μ M;

- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- κ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates (2×10^6 cells/plate) with 16 μ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- κ B-luciferase activity after stimulation with
10 ODN. Four different types of clones were generated.

15 293-hTLR9-luc: expressing human TLR9 and 6-fold NF- κ B-luciferase reporter
293-mTLR9-luc: expressing murine TLR9 and 6-fold NF- κ B-luciferase reporter
293-hTLR9: expressing human TLR9
293-mTLR9: expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20 3×10^6 293T cells were electroporated with 5 μ g NF- κ B-luc plasmid and 5 μ g of either horse TLR9-pcDNA3.1 plasmid or human TLR9-pcDNA3.1 plasmid at 200V, 975 μ F. After the electroporation the cells were plated in 96-well cell culture plates at 2.5×10^4 cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTGTCGTTTGTGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

15

Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

25 All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

Claims

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

5

2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

10 3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

15 4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

5. A vector comprising the nucleic acid of any of claims 3-4.

6. A cell comprising the vector of claim 5.

20

7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.

25 8. A method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:

aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;

30 generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a

15 CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the 20 initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred 30 CpG DNA).

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.
- 5 12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.
13. A vector comprising the nucleic acid of claim 12.
- 10 14. A cell comprising the vector of claim 13.
- 15 15. An antibody that binds specifically to the polypeptide of claim 14.
16. A screening method to identify a TLR9 ligand, comprising:
15 contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;
measuring a signal in response to the contacting; and
identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.
- 20 17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.
- 25 18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF-κB.
19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.
- 30 20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, 5 CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

10 identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

15 23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- κ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20 TCCATGACGTTTGATGTT (SEQ ID NO:39),
TCCATAACGTTTGATGTT (SEQ ID NO:40),
TCCATCACGTTTGATGTT (SEQ ID NO:41),
TCCATTACGTTTGATGTT (SEQ ID NO:42),
TCCATGGCGTTTGATGTT (SEQ ID NO:43),
25 TCCATGCCGTTTGATGTT (SEQ ID NO:44),
TCCATGTCGTTTGATGTT (SEQ ID NO:45),
TCCATGATGTTTGATGTT (SEQ ID NO:46),
TCCATGAAGTTTGATGTT (SEQ ID NO:47),
TCCATGAGGTTTGATGTT (SEQ ID NO:48),
30 TCCATGACATTTGATGTT (SEQ ID NO:49),
TCCATGACCTTTGATGTT (SEQ ID NO:50),
TCCATGACTTTGATGTT (SEQ ID NO:51),
TCCATGACGCTTGATGTT (SEQ ID NO:52),
TCCATGACGATTTGATGTT (SEQ ID NO:53),
35 TCCATGACGGTTTGATGTT (SEQ ID NO:54),
TCCATGACGTCTTGATGTT (SEQ ID NO:55),
TCCATGACGTATTGATGTT (SEQ ID NO:56), and
TCCATGACGTGTTGATGTT (SEQ ID NO:57).

Figure 1
(1/3)

Figure 1
(2/3)

Figure 1
(3/3)

Figure 2

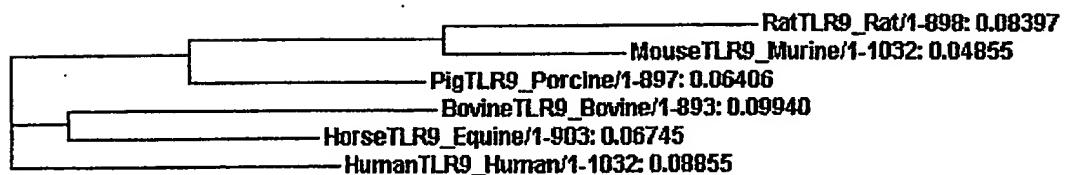
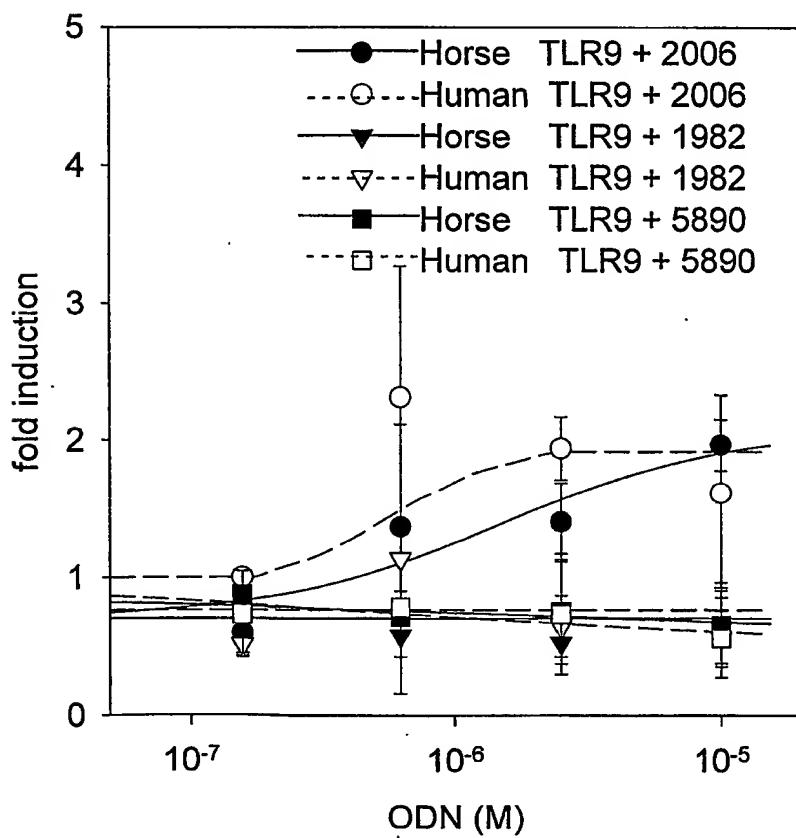


Figure 3



SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH
University of Saskatchewan
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040W000

<150> US 60/412,479
<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1
<211> 1032
<212> PRT
<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610

615

620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Pro Phe Val Asp Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser
805 810 815

Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val
820 825 830

Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln
995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
1025 1030

<210> 2
<211> 821
<212> PRT
<213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe
610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

725

730

735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
 740 745 750

Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly
 755 760 765

Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser
 805 810 815

Arg Asp Cys Phe Gly
 820

<210> 3

<211> 3099

<212> DNA

<213> Rattus norvegicus

<400> 3

atggttctct	gtgcgaggac	cctgcacccc	ttgtctctcc	tggcacaggc	cgcaagtgc	60
gctgaggctc	tggccctggg	taccctgcct	gccttcctac	cctgtgaact	gaagcctcat	120
ggcctggtag	actgcaactg	gtcttcctg	aagtctgtgc	ctcacttctc	tgcgcagaa	180
ccccgttcca	acatcaccag	ccttccttg	atcgccaacc	gcatccacca	cctgcacaac	240
ctcgactttg	tccacactgcc	caacgtgcga	cagctgaacc	tcaagtggaa	ctgtccgccc	300
cctggcctca	gcccccttgca	cttctcctgc	cgcacatgacca	ttgagccaa	aaccttcctg	360
gctatgcgca	tgcttggaa	gctgaacctg	agctataacg	gtatcaccac	tgtgcggccc	420
ctgcccagct	ccctgacgaa	tctgagccta	agccacacca	acatcctggt	actcgatgcc	480
agcagcctcg	ctggcctgca	cagcctgcga	gttctttca	tggacggaa	ctgctactac	540
aagaacccct	gcaacggggc	ggtgaacgtg	accccggaacg	ctttcctggg	cttgagcaac	600
ctcaccctact	tgtcccttaa	gtataacaac	ctcacagagg	tgcggcgcca	actgcggccc	660
agcctggagt	acctcctgct	gtcctataac	ctcatcgta	agctgggggc	cgaagaccta	720
gccaacctga	cctcccttcg	aatgcttgat	gtgggtggga	attgccgtcg	ctgtgatcac	780

gccccggacc	tctgtacaga	atgcggcag	aagtcccttg	atctgcaccc	tcagactttc	840
catcacctga	gccaccttga	aggcctggtg	ctgaaggaca	gttctctcca	ctcgctgaac	900
tccaaagtgg	tccagggtct	ggcgaacctc	tcggtgctgg	acctaagcga	gaactttctc	960
tacgagagca	tcaacaaaac	cagcgcctt	cagaacctga	cccgtctgctg	caagctcgac	1020
ctgtccctca	attactgcaa	gaaggatcg	ttcgcccgcc	tccacctggc	aagttccttc	1080
aagagcctgg	tgtcgctgca	ggagctgaac	atgaacggca	tcttcttccg	cttactcaac	1140
aagaacacgc	tcaggtggct	ggctggctcg	cccaagctcc	acacgctgca	ccttcaaattg	1200
aatttcatca	accaggcgca	gctcagcgctc	tttagtacct	tccgagccct	tgcgtttgtg	1260
gacctgtcca	ataatcgcat	cagcggccct	ccaaacgctgt	ccagagtcgc	ccccgaaaag	1320
gcagacgagg	cggagaaggg	ggttccatgg	cctgcaagtc	tcaccccagc	tctcccgagc	1380
actcccgct	caaagaactt	catggtcagg	tgtaagaacc	tcagattcac	catggacctg	1440
tctcggaaca	accaggtgac	tatcaagcca	gagatgttcg	tcaacctctc	ccatctccag	1500
tgtctgagcc	tgagccacaa	ctgcatcgctg	caggctgtca	atggctctca	gttcctgccc	1560
ctgaccaacc	tgaagggtgct	ggacctgtcc	tataacaagc	tggacctgta	ccattcgaaa	1620
tcgttcaagt	agctcccaca	gttgcaggcc	ctggacctga	gctacaacag	ccagccattc	1680
agcatgcagg	ggataggcca	caacttcagt	tttctggcca	atctgtccag	gttacagaac	1740
cttagcctgg	cacacaatga	cattcacagc	cgcgtgtcct	cacgcctcta	cagcacctca	1800
gtggagttatc	tggacttcag	cggcaacgg	gtggccgca	tgtggacgca	ggaggacctt	1860
tacctctatt	tcttccaaga	cctgagaagc	ctgattcatc	tggacctgtc	tcagaataag	1920
ctgcacatcc	tccggcccca	gaacctcaac	tacccccc	agagcctgac	gaagctgagt	1980
ttccgtgaca	atcacctctc	tttcttaac	tggagcagtc	tggccttcct	gcccaatctg	2040
cgagacctgg	acctggcagg	caatctacta	aaggccctga	ccaaacggcac	cctgcctaatt	2100
ggcacgtcc	tccagaaaact	ggatgtcagt	agcaacagta	tcgtctttgt	ggtcccagcc	2160
ttctttgtc	tggcggtaga	gtctaaaagag	gtcaacctca	gccataacat	cctcaagact	2220
gtggatcgct	cctgggtttgg	gcccattgt	atgaacctga	cggttctaga	cgtgagcagc	2280
aaccctctgc	attgtgcctg	cggtgacccc	ttttagact	tactgctgga	agtgcagacc	2340
aaggtgcctg	gcctggctaa	cggtgtgaag	tgtggcagtc	cccgccagct	gcagggccgc	2400
agcatcttg	cgcaagacct	cgggctgtgc	ctggatgacg	tcctttctcg	ggactgcttt	2460
ggcctttcac	tcctggctgt	ggccgtgggc	acggtgttgc	ctttactgca	gcacatctgc	2520
ggctgggacg	tctggtactg	tttccatctg	tgccctggcat	ggctacctt	gctgaccctgt	2580

ggccggcgca	gcccggca	gcgcggca	tctcccttat	gatgccttcg	tggtgttcga	taaggcgca	2640
agcgcgggtt	ctgactgggt	gtataacgag	cttcgagtgc	ggctagagga	gcggcgccgt		2700
cgccgagccc	taegcttgtg	tctggaggac	cgagattggc	tgccctggca	gacactcttc		2760
gagaacctct	gggcctccat	ctatggcagc	cgcaagactc	tgtttgtgct	ggcccacacg		2820
gacaagggtca	gtggcctcct	gcccggccagc	ttcctgctgg	ctcagcagcg	cctgctggag		2880
gaccgcaagg	acgtgggtgg	gttggtgatc	ctgcgcctg	atgcccacacg	ctccccgtac		2940
gtgcgactgc	gccagcgcct	ctgcccggcag	agtgtgtct	tctggcccca	tcagcccaac		3000
ggcaggggca	gcttctggc	ccagctgagt	acagccctga	ctagggacaa	ccaccacttc		3060
tataaccgga	acttctgccc	gggacctaca	gcagaatag				3099

<210> 4
 <211> 2463
 <212> DNA
 <213> Rattus norvegicus

<400> 4	atggttctct	gtcgcaggac	cctgcacccccc	ttgtctctcc	tggtacaggc	cgcagtgcgt	60
	gctgaggctc	tggccctggg	taccctgcct	gccttcctac	cctgtgaact	gaaggcctcat	120
	ggcctggtag	actgcaactg	gctcttcctg	aagtctgtgc	ctcacttctc	tgccgcagaa	180
	ccccgttcca	acatcaccag	ccttccttgc	atcgccaaacc	gcatccacca	cctgcacaac	240
	ctcgactttg	tccacctgcc	caacgtgcga	cagctgaacc	tcaagtggaa	ctgtccggccc	300
	cctggcctca	gccccttgca	cttctcctgc	cgcatgacca	ttgagcccaa	aactttcctg	360
	gctatgcgca	tgctggaaga	gctgaacctg	agctataacg	gtatcaccac	tgtgccccgc	420
	ctgcccagct	ccctgacgaa	tctgagccta	agccacacca	acatcctgg	actcgatgcc	480
	agcagcctcg	ctggcctgca	cagcctgcga	gttctttca	tggacggaa	ctgctactac	540
	aagaacccct	gcaacggggc	ggtgaacgtg	acccggacg	ctttcctggg	cttgagcaac	600
	ctcacccact	tgtcccttaa	gtataacaac	ctcacagagg	tgcggccca	actgcccccc	660
	agcctggagt	acccctgtct	gtcctataac	ctcatcgta	agctgggggc	cgaagaccta	720
	gccaacctga	cctcccttcg	aatgcttgat	gtgggtggga	attgccgtcg	ctgtgatcac	780
	gccccccgacc	tctgtacaga	atgcggcag	aagtcccttg	atctgcaccc	tcagactttc	840
	catcacctga	gccaccttga	aggcctggtg	ctgaaggaca	gttctctcca	ctcgctgaac	900
	tccaagtgg	tccagggtct	ggcgaacctc	tggtgctgg	acctaagcga	gaactttctc	960
	tacgagagca	tcaacaaaac	cagcgccctt	cagaacctga	cccgctcg	caagctcgac	1020

ctgtccttca	attactgcaa	gaaggtatcg	ttcgcccgcc	tccacctggc	aagttccttc	1080
aagagcctgg	tgtcgctgca	ggagctgaac	atgaacggca	tcttcttccg	cttactcaac	1140
aagaacacgc	tcaggtggct	ggctggctcg	cccaagctcc	acacgctgca	ccttcaaatg	1200
aatttcatca	accaggcgca	gctcagcgtc	tttagtacct	tccgagccct	tcgctttgtg	1260
gacctgtcca	ataatcgcat	cagcgggcct	ccaacgctgt	ccagagtgc	ccccgaaaag	1320
gcagacgagg	cggagaaggg	ggttccatgg	cctgcaagtc	tcaccccagc	tctcccgagc	1380
actcccgtct	caaagaactt	catggtcagg	tgttagaacc	tcagattcac	catggacctg	1440
tctcggaaaca	accaggtgac	tatcaagcca	gagatgttcg	tcaacctctc	ccatctccag	1500
tgtctgagcc	tgagccacaa	ctgcacatcg	caggctgtca	atggctctca	gttcctgccc	1560
ctgaccaacc	tgaagggtgct	ggacctgtcc	tataacaagc	tggacctgta	ccattcgaaa	1620
tcgttcagtg	agctcccaca	gttgcaggcc	ctggacctga	gctacaacag	ccagccattc	1680
agcatgcagg	ggataggcca	caacttcagt	tttctggcca	atctgtccag	gttacagaac	1740
cttagcctgg	cacacaatga	cattcacagc	cgcgtgtcc	cacgcctcta	cagcacctca	1800
gtggagttatc	tggacttcag	cggcaacgggt	gtggggccgca	tgtgggacga	ggaggacctt	1860
tacctctatt	tcttccaaga	cctgagaagc	ctgattcatac	tggacctgtc	tcagaataag	1920
ctgcacatcc	tccggcccca	gaacctaaca	tacccccc	agagcctgac	gaagctgagt	1980
ttccgtgaca	atcacctctc	tttcttaac	tggagcagtc	tggccttcct	gcccaatctg	2040
cgagacctgg	acctggcagg	caatctacta	aaggccctga	ccaaacggcac	cctgcctaatt	2100
ggcacgctcc	tccagaaact	ggatgtcagt	agcaacagta	tgcgtttgt	ggtcccagcc	2160
ttctttgttc	tggcggtaga	gtaaaagag	gtcaacctca	gccataacat	cctcaagact	2220
gtggatcgct	cctggtttgg	gcccattgtg	atgaacctga	cggttctaga	cgtgagcagc	2280
aaccctctgc	attgtgcctg	cggtgacacc	ttttagact	tactgctgga	agtgcagacc	2340
aagggtgcctg	gcctggctaa	cggtgtgaag	tgtggcagtc	cccgccagct	gcagggccgc	2400
agcatctttg	cgcaagacct	gcccgtgtgc	ctggatgacg	tcccttcctg	ggactgcttt	2460
ggc						2463

<210> 5
 <211> 1030
 <212> PRT
 <213> Sus scrofa

<400> 5

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Cys Ile Thr Lys Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705	710	715	720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu			
725	730	735	
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys			
740	745	750	
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr			
755	760	765	
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro			
770	775	780	
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile			
785	790	795	800
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn			
805	810	815	
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro			
820	825	830	
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu			
835	840	845	
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala			
850	855	860	
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val			
865	870	875	880
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg			
885	890	895	
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro			
900	905	910	
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg			
915	920	925	
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu			
930	935	940	

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys
945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg
965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp
980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr
995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys
1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu
1025 1030

<210> 6
<211> 819
<212> PRT
<213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
1 5 10 15

Thr Ala Leu Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Cys Ile Thr Lys Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe
705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu
725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys
740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr
755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro
770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile
785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn
805 810 815

Cys Phe Gly

<210> 7
 <211> 3352
 <212> DNA
 <213> Sus scrofa

<400> 7	
gagcacgaac atccttcaact gtagctgctg cccggctatgc cagccagacc ctttggagaa	60
gaccccaactc cctgtcatgg gcccccgctg caccctgcac ccccttctc tcctggtgca	120
ggtgacagcg ctggctgcgg ctctggccca gggcaggctg cctgccttcc tgccctgtga	180
gctccagccc cacggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt	240
ctcggcggca gcgccccggg ccaacgtcac cagccctctcc ttactctcca accgcacatcca	300
ccacacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctaagtg	360
gaactgcccgg cggctggcc tcagccccat gcacttcccc tgccacatga ccatcgagcc	420
caacaccccttc ctggccgtgc ccaccctgga ggagctgaac ctgagctaca acagcatcac	480
gaccgtgcct gcctgtcccg actccctcgt gtccctgtcg ctgagccgca ccaacatcct	540
ggtgctagac cccaccccacc tcactggcct acatgcctg cgctacctgt acatggatgg	600
caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgcctcct	660
cggcctggc aacctcacac atctctcaact caagtacaac aatctcacgg aggtgccccgg	720
cagcctgccc cccagcctgg agaccctgct gttgtctac aaccacatttgc tcaccctgac	780
gcctgaggac ctggccaatc tgactgcctt ggcgtgtctt gatgtggggg ggaactgccc	840
ccgctgtgac catgccccca accccctgcag ggagtgcaca aaggaccacc ccaagctgca	900
ctctgacacc ttcagccacc tgagccctt cgaaggcctg gtgttgaag acagttctct	960
ctacaacctg gacaccagggt gttccgagg cctggacagg ctccaagtgc tggacctgag	1020
tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggcccgact	1080
gcccggccctt aacctgtcct tcaattacca caagaagggt tcctttgccc acctgcacct	1140
ggcaccctcc tttgggcacc tccggccctt gaaggagctg gacatgcatttgc gcatcttctt	1200
ccgctcgctc agttagacca cgctccaaacc tctggtccaa ctgcctatgc tccagaccct	1260
gcccgtgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg cttccctgg	1320
cctgctgtac gtggacctat cggacaacccg catcagcgga gctgcaaggc cagtggccat	1380
tactagggag gtggatggta gggagagggt ctggctgcct tccaggaacc tcgctccacg	1440
tccactggac actctccgct cagaggactt catgccaaac tgcaaggcct tcagcttac	1500

cttggacctg tctcggaaca acctggtgac aatccagtcg gagatgttg ctcgcctctc 1560
 acgcctcgag tgccctgcgcc tgagccacaa cagcatctcc caggcggtca atggctctca 1620
 gtttgtggcg ctgaccagcc tgccgggtgct ggacctgtcc cacaacaagc tggacctgt 1680
 tcacgggcgc tcgttcacgg agctgcccgc cctggaagca ctggacctca gctacaatag 1740
 ccagcccttt accatgcagg gtgtgggcca caacctcagc ttctgtggcc agctgcccgc 1800
 cctgcgctac ctcagcctgg cgcacaatga catccatagc cgagtgtccc agcagctctg 1860
 tagcgctca ctgtgcgccc tggactttag cggcaacgat ctgagccgga tgtggctga 1920
 gggagacctc tatctccgct tcttccaagg cctaaagaagc ctatgttgc tggacctgtc 1980
 ccagaaccac ctgcacaccc tcctgccacg tgccctggac aacctccccaa aaaggcctgaa 2040
 gcatctgcat ctccgtgaca ataaccttgc cttcttcaac tggagcagcc tgaccctct 2100
 gcccaagctg gaaaccctgg acttggctgg aaaccagctg aaggccctaa gcaatggcag 2160
 cctgcacatct ggcacccagc tgccggaggct ggacctcagt ggcaacagca tcggctttgt 2220
 gaaccctggc ttctttgccc tggccaagca gttagaagag ctcaacctca ggcaccaatgc 2280
 cctcaagaca gtggagccct cctgggttgg ctgcgtggc ggcaacctga aagtccctaga 2340
 cgtgagcgc aaccctctgc actgtgcctg tggggcgacc ttctgtggct tcctgttgg 2400
 ggtacaggct gccgtgcctg ggctgcccag ccgcgtcaag tgtggcagtc cggggcagct 2460
 ccagggccat agcatctttg cgcaagaccc tgcgcctctgc ctggatgaga ccctctcg 2520
 gaactgtttt ggcacatctcg tgcgtggccat ggccctggc ctggttgtgc ccatgtcg 2580
 ccacctctgc ggctgggacc tctggtaactg cttccacctg tgccctggct ggctgcccc 2640
 cggaggccag cggcggggcg cagacccct gttctatgtat gccttcgtgg tctttgacaa 2700
 agctcagagt gctgtggccg actgggtgtt caacgagctg cgggtgcagc tggaggagcg 2760
 ccgtggccgc cgccgtactgc gcctgtgcct ggaggagcga gactggttac ctggcaagac 2820
 gctcttcgag aaccctgtggg cctcagtcta cagcagccgc aagaccctgt ttgtgtggc 2880
 ccacacggac cgtgtcagcg gcctcttgcg tgccagtttc ctgctggccc agcagcgcct 2940
 gctggaggac cgcaaggacg ttgttagtgc ggtgatcctg cgcccccagatg cctaccgtc 3000
 ccgctacgtg cggctgcgc agcgcctctg ccgcagact gtcctccct ggccccacca 3060
 gccccgtggg cagggcagct tctggggccca gctgggcaca gccctgacca gggacaacca 3120
 ccacttctat aaccggaaact tctgcggggg ccccacgaca gccgaatagc actgagtgac 3180
 agcccaagttg ccccaagccccc cctggatttg cctctctgccc tgggggtggccc caaccctgtt 3240
 tgctcagcca caccactgct ctgcctccctg ttccccaccc caccggccag cctggcatgt 3300

aacatgtgcc	caataaaatgc	taccggaggg	ccaagaaaaaa	aaaaaaaaaa	aa	3352
<210>	8					
<211>	2457					
<212>	DNA					
<213>	Sus scrofa					
<400>	8					
atggggccccc	gctgcaccct	gcacccctt	tctctcctgg	tgcaggtgac	agcgctggct	60
gccccatctgg	cccaggcag	gctgcctgcc	ttcctgcctt	gtgagctcca	gccccacggc	120
ctgggtgaact	gcaactggct	cttcctgaag	tccgtgcccc	acttctcgcc	ggcagcgccc	180
cggggccaacg	tcaccagcct	ctccttactc	tccaaaccgca	tccaccacct	gcacgactcc	240
gacttctgtcc	acctgtccag	cctacgaact	ctcaacactca	agtggaaactg	cccgccggct	300
ggcctcagcc	ccatgcactt	cccctgccac	atgaccatcg	agcccaacac	cttcctggcc	360
gtgcccaccc	tggaggagct	gaacctgagc	tacaacagca	tcacgaccgt	gcctgccttg	420
cccgactccc	tcgtgtccct	gtcgctgagc	cgcaccaaca	tcctgggtct	agacccacc	480
cacccactg	gcctacatgc	cctgcgtac	ctgtacatgg	atggcaactg	ctactacaag	540
aacccctgcc	agggggcgct	ggaggtggtg	ccgggtgccc	tcctggcct	ggcaacctc	600
acacatctct	cactcaagta	caacaatctc	acggaggtgc	ccgcagccct	gccccccagc	660
ctggagaccc	tgctgttgtc	ctacaaccac	attgtcaccc	tgacgcctga	ggacctggcc	720
aatctgactg	ccctgcgcgt	gcttgatgtg	ggggggact	gcccgcgtg	tgaccatgcc	780
cgcaacccct	gcagggagtg	cccaaaggac	caccccaagc	tgcactctga	cacccctcagc	840
cacctgagcc	gcctcgaagg	cctgggtttg	aaagacagtt	ctctctacaa	cctggacacc	900
aggtggttcc	gaggcctgga	caggctccaa	gtgctggacc	tgagtgagaa	cttcctctac	960
gactgcata	ccaagaccac	ggccttccag	ggcctggccc	gactgcgcag	cctcaacctg	1020
tccttcaatt	accacaagaa	ggtgtccttt	gcccacctgc	acctggcacc	ctcctttggg	1080
cacctccgg	ccctgaagga	gctggacatg	catggcatct	tcttccgcctc	gctcagttag	1140
accacgctcc	aacctctgg	ccaaactgcct	atgctccaga	ccctgcgcct	gcagatgaac	1200
ttcattaacc	aggcccagct	cagcatcttt	ggggccttcc	ctggcctgct	gtacgtggac	1260
ctatcgac	accgcacatcg	cggagctgca	aggccagtgg	ccattactag	ggaggtggat	1320
ggtagggaga	gggtctggct	gccttccagg	aacctcgctc	cacgtccact	ggacactctc	1380
cgctcagagg	acttcatgcc	aaactgcaag	gccttcagct	tcaccttgg	cctgtctcgg	1440
aacaacctgg	tgacaatcca	gtcggagatg	tttgctgcct	tctcacgcct	cgagtgcctg	1500

cgcctgagcc acaacagcat	ctcccaggcg	gtcaatggct	ctcagttgt	gcccgtgacc	1560	
agcctgcggg	tgctggacct	gtcccacaac	aagctggacc	tgtatcacgg	gcgctcggtc	1620
acggagctgc	cgccctgga	agcaactggac	ctcagctaca	atagccagcc	ctttaccatg	1680
cagggtgtgg	gccacaacct	cagttcgtg	gcccagctgc	ccgcccgtcg	ctacctcagc	1740
ctggcgcaca	atgacatcca	tagccgagtg	tcccagcgc	tctgtagcgc	ctcaactgtgc	1800
gccctggact	ttagcggcaa	cgatctgagc	cgatgtggg	ctgagggaga	cctctatctc	1860
cgcttcttcc	aaggcctaag	aagcctagtc	tggctggacc	tgtcccagaa	ccacctgcac	1920
accctcctgc	cacgtgcct	ggacaacctc	cccaaaagcc	tgaagcatct	gcatctccgt	1980
gacaataacc	tggccttctt	caactggagc	agcctgaccc	tcctgccccaa	gctggaaacc	2040
ctggacttgg	ctggaaacca	gctgaaggcc	ctaagcaatg	gcagcctgcc	atctggcacc	2100
cagctgcgga	ggctggacct	cagtggcaac	agcatcggt	ttgtgaaccc	tggcttcttt	2160
gccctggcca	agcagttaga	agagctcaac	ctcagcgcca	atgcccctcaa	gacagtggag	2220
ccctcctgg	ttggctcgat	ggtggcaac	ctgaaaagtcc	tagacgtgag	cgccaaaccct	2280
ctgcactgtg	cctgtggggc	gaccttcgtg	ggcttcctgc	tggaggtaca	ggctgccgtg	2340
cctggctgc	ccagccgcgt	caagtgtggc	agtccgggc	agctccaggg	ccatagcatc	2400
tttgcgcaag	acctgcgcct	ctgcctggat	gagaccctct	cgtggaaactg	ttttggc	2457

<210> 9
 <211> 1029
 <212> PRT
 <213> Bos taurus

<400> 9

Met	Gly	Pro	Tyr	Cys	Ala	Pro	His	Pro	Leu	Ser	Leu	Leu	Val	Gln	Ala
1					5				10				15		

Ala	Ala	Leu	Ala	Ala	Leu	Ala	Glu	Gly	Thr	Leu	Pro	Ala	Phe	Leu
							25				30			

Pro	Cys	Glu	Leu	Gln	Pro	His	Gly	Gln	Val	Asp	Cys	Asn	Trp	Leu	Phe
					35			40			45				

Leu	Lys	Ser	Val	Pro	His	Phe	Ser	Ala	Gly	Ala	Pro	Arg	Ala	Asn	Val
					50			55			60				

Thr	Ser	Leu	Ser	Leu	Ile	Ser	Asn	Arg	Ile	His	His	Leu	His	Asp	Ser
					65			70			75		80		

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr

305	310	315	320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg			
325	330	335	
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His			
340	345	350	
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu			
355	360	365	
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln			
370	375	380	
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn			
385	390	395	400
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu			
405	410	415	
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro			
420	425	430	
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu			
435	440	445	
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp			
450	455	460	
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn			
465	470	475	480
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu			
485	490	495	
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly			
500	505	510	
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His			
515	520	525	
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln			
530	535	540	

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg
930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala
995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
1010 1015 1020

Gly Pro Thr Thr Ala Glu
1025

<210> 10
<211> 818
<212> PRT
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln
370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420 425 430

Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
 805 810 815

Phe Gly

<210> 11
 <211> 3191
 <212> DNA
 <213> Bos taurus

<400> 11			
gggaagtggg cgccaaagcat cttccctgc agctgcctcc caacctgccc gccagaccct	60		
ctggagaagc cgcattccct gtcatggcc cctactgtgc cccgcacccc ctttctctcc	120		
tggtgccaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttctgc	180		
cctgtgagct ccagccccat ggtcaggtgg actgcaactg gctgttcctg aagtctgtgc	240		
cgcacttttc ggctggagcc ccccgccca atgtcaccag cctctccctta atctccaacc	300		

gcatccacca	cttgcacatgac	tctgacttcg	tccacacctg	caacacctgcgg	gtcctcaacc	360
tcaagtgaa	ctgccccgg	gccggcctca	gccccatgca	cttcccctgc	cgtatgacca	420
tcgagccaa	cacccatcctg	gctgtgccc	ccctggagga	gctgaacctg	agctacaacg	480
gcatcacgac	cgtgcctg	ccctccagtt	ccctcgtg	cctgtcg	agccacacca	540
gcatccgtt	gctaggcccc	acccacttca	ccggcctgca	cggcctgcgc	tttctgtaca	600
tggacggcaa	ctgctactac	atgaaccctt	gccccggggc	cctggagg	gccccaggcg	660
ccctccctcg	cctggcaac	ctcacgcacc	tgtcgctcaa	gtacaacaac	ctcacggagg	720
tgccccggc	cctggccccc	agcctggaca	ccctgctg	gtcctacaac	cacattgtca	780
ccctggcacc	cgaggacctg	gccaacctga	ctggccctg	cgtgcttg	gtgggtggg	840
actggcccg	ctgcgaccat	gcccgaacc	cctgcagg	gtgccc	aaag aacttcccc	900
agctgcaccc	tgacaccc	agtgcac	gccc	gtgccc	aaag aacttcccc	960
gttctctcta	caaactagag	aaagattgg	tccgcgg	gggcagg	ctca	1020
acctgagtga	gaacttc	tatgactaca	tcaccaagac	caccat	ttgcac	1080
cccagctg	cagactcaac	ctgtc	attaccacaa	gaagg	gttgc	1140
tgcacctagc	gtcctc	tttggg	tgtcc	gaag	gttgc	1200
tcttcttccg	ctccctc	accatc	tccag	gttgc	gacccgg	1260
agagtctgca	tctgc	acttca	accagg	gttgc	gttggg	1320
tcccggcct	gcttc	tcgg	acaacc	gttgc	gttggg	1380
cggccgcct	ggggg	gagg	gacag	gttgc	gttggg	1440
ctccaggccc	gttgc	acttca	aggactt	gttgc	gttggg	1500
tcaccttgg	cctgt	caac	tttacc	gttgc	gttggg	1560
tctccgcct	ccagt	tcgt	ccat	gttgc	gttggg	1620
cccagttcg	gccc	gttgc	acc	gttgc	gttggg	1680
tgtaccatgg	gccc	gttgc	acttgc	gttgc	gttggg	1740
acagccagcc	tttc	catg	cagg	gttgc	gttggg	1800
cctccctgcg	ctac	ctc	atgg	gttgc	gttggg	1860
tcagcagcgc	ctcg	ttgc	ccctgg	tcag	gttggg	1920
ccgagggaga	cctctat	tc	tttca	aagg	gttgg	1980
tgtccgagaa	ccat	ctgcac	acc	ctgcac	ggacaac	2040

tgccgcagct	gcgtctccgg	gacaataacc	tggccttctt	caactggagc	agcctgaccg	2100
tcctgccccg	gctggaagcc	ctggatctgg	cagaaacca	gctgaaggcc	ctgagcaacg	2160
gcagcctgcc	gcctggcatc	cggtccaga	agctggacgt	gagcagcaac	agcatcggt	2220
tcgtgatccc	cggcttcttc	gtccgcgca	ctcggctgat	agagcttaac	ctcagcgcca	2280
atgcctgaa	gacagtggat	ccctccttgt	tcggttcctt	agcagggacc	ctgaaaatcc	2340
tagacgtgag	cggcaacccg	ctccactgca	cctgcggggc	ggcccttgc	gacttcctgc	2400
tggagagaca	ggaggccgtg	ccggggctgt	ccagggcggt	cacatgtggc	agtccgggccc	2460
agctccaggg	ccgcagcatc	ttcacacagg	acctgcgcct	ctgcctggat	gagaccctct	2520
ccttggactg	ctttggcttc	tcactgctaa	tggtggcgct	gggcctggca	gtgcccattgc	2580
tgcaccaccc	ctgtggctgg	gacctcttgt	actgcttcca	cctgtgtctg	gcccatttgc	2640
cccgacggcg	gccccggcgg	ggcgaggaca	ccctgctcta	tgtgcgcgtc	gtggcttgc	2700
acaagggtgca	gagtgcagtg	gctgattggg	tgtacaacga	gctccgcgtg	cagctggagg	2760
agcgccgggg	gccccggggcg	ctccgcctct	gcctggagga	gcgagactgg	ctccctggta	2820
agacgctctt	cgagaacctg	tgggcctcgg	tctacagcag	ccgcaagacc	atgttcgtgc	2880
tggaccacac	ggaccgggtc	ageggcctcc	tgccgcgcag	cttcctgtcg	gcccagcagc	2940
gcctgttgg	ggaccgcgaa	gacgtcgtag	tgctggtgat	cctgcgccttcc	gcccctatc	3000
ggtcccgcta	cgtgcggctg	cgccagcgcc	tctgcgccttca	gagcgtcctc	ctctggccccc	3060
accagccca	tggccagggt	agtttctggg	ccaacctggg	catagccctg	accagggaca	3120
acggtaactt	ctataaccgg	aacttctgcc	ggggcccccac	gacagccgaa	tagcacagag	3180
tgactgcccc	g					3191

<210> 12
 <211> 2454
 <212> DNA
 <213> Bos taurus

<400> 12	atggccccc	actgtgcccc	gcacccctt	tctctcctgg	tgcaggccgc	ggcactggca	60
	ggcccttgg	ccgagggcac	cctgcctgcc	ttcctgcctt	gtgagctcca	gccccatgg	120
	cagggtggact	gcaactggct	gttcctgaag	tctgtgcgc	acttttccgc	tggagccccc	180
	cgcccaatg	tcaccagct	ctcccttaatc	tccaaaccgca	tccaccactt	gcatgactct	240
	gacttcgtcc	acctgtccaa	cctgcgggtc	ctcaacctca	agtggaaactg	cccgccggcc	300
	ggcctcagcc	ccatgcactt	cccctgccgt	atgaccatcg	agcccaacac	tttcctggct	360

gtgcccaccc	tggaggagct	gaacctgagc	tacaacggca	tcacgaccgt	gcctgccctg	420
cccagttccc	tcgtgtccct	gtcgctgagc	cacaccagca	tcctggtgct	aggccccacc	480
cacttcacccg	gcotgcacgc	cctgcgcctt	ctgtacatgg	acggcaactg	ctactacatg	540
aaccctgcc	cgcgggccc	ggaggtggcc	ccaggcgccc	tcctcggcct	gggcaacctc	600
acgcacctgt	cgtcaagta	caacaacctc	acggaggtgc	cccgccgcct	gccccccagc	660
ctggacaccc	tgctgctgtc	ctacaaccac	attgtcacc	tggcacc	ggac	720
aacctgactg	ccotgcgcgt	gcttgacgtg	ggtgggaact	gccgcgcgt	cgaccatgcc	780
cgcaacccct	gcagggagtg	cccaaagaac	ttccccaagc	tgcac	ctga	840
cacctgagcc	gcotcgaagg	cctgggttt	aaggacagtt	ctctctacaa	actagagaaa	900
gattggttcc	gcggcctggg	caggctcaa	tgctcgacc	tgagt	gagaa	960
gactacatca	ccaagaccac	catcttcaac	gac	ctgc	actcaac	1020
tccttcaatt	accacaagaa	ggtgtcc	gc	ccac	ctgc	1080
agtctggtgt	ccctggagaa	gctggacatg	cacggcat	tcttc	gc	1140
atcacgctcc	agtgcgtgac	ccggctgccc	aag	cttc	gac	1200
ttcatcaacc	aggcccagct	cagcat	ttt	ggc	ttt	1260
ctgtcgac	accgc	atc	ggcc	cc	gg	1320
agcaggg	ttt	gg	gg	cc	gg	1380
agctcaaagg	acttcatg	caac	c	ttgg	ac	1440
aacctgg	ttt	ccatcc	cc	gg	gg	1500
ctgagccaca	acagcat	ctc	ggcg	cc	gg	1560
ctgcag	ttt	ccaca	cc	gg	cc	1620
gagctg	cc	aca	cc	gg	cc	1680
ggcgt	cc	aa	cc	cc	cc	1740
g	cc	aa	cc	cc	cc	1800
ctggacttca	gcggcaactc	cctgagccag	atgtggcc	agg	gagac	1860
ttttcaaa	g	cttgg	ccag	cc	ttt	1920
ctcctgc	c	ttt	gg	cc	ttt	1980
aataac	ttt	cc	gg	cc	ttt	2040
gatctgg	cc	ttt	cc	gg	cc	2100
ctccaga	gg	ttt	cc	gg	cc	2160
ac	cc	ttt	cc	gg	cc	

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220
 tcctggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caacccgctc 2280
 cactgcgcct gcggggcggc ctttgtggac ttcctgctgg agagacagga ggccgtgccc 2340
 gggctgtcca ggccgtcac atgtggcagt ccgggccagc tccagggccg cagcatctc 2400
 acacaggacc tgccctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13
 <211> 1031
 <212> PRT
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp
850 855 860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

865

870

875

880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
 995 1000 1005

Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe
 1010 1015 1020

Cys Arg Gly Pro Thr Met Ala Glu
 1025 1030

<210> 14
 <211> 820
 <212> PRT
 <213> Equus caballus

<400> 14

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu

35

40

45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
 260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
 805 810 815

Asp Cys Phe Gly
 820

<210> 15
<211> 3391
<212> DNA
<213> Equus caballus

<400> 15
ctctgttctc tgagctgttg ccgcgtgaag ggactgcgag cacaaagcat cctcctctgc 60
agctgctgcc cagtgtgcc a gctggaccct ctggatcatc tcccactccc tgtcatggc 120
ccttgccatg gtgccctgca gcccctgtct ctccctggc aggcggccat gctggccgtg 180
gctctggccc aaggcaccct gcctcccttc ctgcccgtg agctccagcc ccacggcctg 240
gtgaactgca actggctgtt cctgaagtcc gtgc cccact tctcagcagc agcaccgg 300
gacaatgtca ccagccttcc ttgctctcc aaccgcattc accacccatca cgactccgac 360
tttgcccaac tgtccaaacct gcagaaactc aacccatcaat ggaactgccc gccagccggc 420
ctcagccca tgcacttccc ctgccacatg accatcgagc ccaacacttt cctggctgta 480
cccaccctgg agtagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc 540
agctccctcg tgtccctgat cctgagccgc accaacatcc tgcagctaga cccaccaggc 600
ctcacgggcc tgcattccct ggcattccata tacatggatg gcaactgcta ctacaagaac 660
ccctgcgggc gggccctgga ggtggccccc ggcgcctcc ttggcctggg caacccatcc 720
cacctgtcac tcaagtacaa caacccatca acgggtccccc gcagcctgcc ccctggctg 780
gagtagctgc tggatgtccata caaccacatt gtcaccctgg cacctgagga cctggccat 840
ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgccc ggcgctgtga ccatgcacgc 900
aaccctgctgac tggagtgcac acataaaatcc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaaga	1020
tggttccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaacct cctctacgac	1080
tgcacatcacca aaaccaaggc attccagggc ctggcccagc tgcaagact caacttgtcc	1140
ttcaattacc ataagaaggt gtccttcgcc cacotgacgc tggcaccctc cttcgggagc	1200
ctgctctccc tgcaggaact ggacatgcat ggcacatctct tccgctcaact cagccagaag	1260
acgctccagc cactggcccg cctgcccattg ctccagcgctc tgtatctgca gatgaacttc	1320
atcaaccagg cccagctcggt catcttcaag gacttccctg gtctgcgcta catagacctg	1380
tcaagacaacc gcatcagtgg agctgtggag ccgggtggcca ccacagggga ggtggatgg	1440
ggaaagaagg tctggctgac atccaggac ctcactccag gcccactgga caccggcagc	1500
tctgaggact tcatgccaag ctgcaagaac ctcagcttca ccttggacct gtcacggAAC	1560
aacctggtaa cagtccagcc agagatgttt gcccagctct cgcgcctcca gtgcctgcgc	1620
ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc	1680
ctgcagggtgc tggacctgtc ccataacaaa ctggacctgt accatggcgctcgttacg	1740
gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg	1800
ggtgtggcc acaacctcag ctttgtggcc cagctgccc ccctgcgcta cctcagcctg	1860
gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtggcc	1920
ctggacttca gcggcaattc cctgagccag atgtggctg agggagacct ctatccgc	1980
ttcttccaag gcctgagaag cctaattccgg ctagacctgt cccagaatcg tctgcataacc	2040
ctcctgccat gcacccctggg caacccccc aagagcttgc agctgctgctg tctccgttaac	2100
aattacctgg ctttcttcaa ttggagcagc ctgaccctcc tgcccaacct ggaaaccctg	2160
gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcacccag	2220
ctccagagggc tggacgtcag caggaacagc atcatcttgc tggccctgg cttctttgct	2280
ctggccacga ggctgcgaga gctcaaccc agtgccaaacg ccctcaggac agaggagccc	2340
tcctggtttgc ttcccttagc aggctccctt gaagtccttag atgtgagcgc caaccctctg	2400
cactgcgcct gtggggcagc ctttgtggac ttccctgctgc aggttcaggc tgccgtgcct	2460
ggtctgccc gcccgtcaa gtgtggcagt ccggccagc tccagggccg cagcatctc	2520
gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctctca	2580
ttgctggttg tggccctggg cctggccatg cctatgttgc accacacttg cggctggac	2640
ctctggtaact gcttccaccc gggcctggcc tggctgcccc ggcgggggtg gcagcggggc	2700

gcggatgcc	tgagctatga	tgcccttgc	gtttcgaca	aggcacagag	cgcagtggcc	2760
gactgggtgt	acaatgaact	gcgggtgcgg	ctagaggagc	gccgtggcg	ccggcgctc	2820
cgcctgtgtc	tggaggagcg	tgactggcta	cctggcaaga	cgctgttgc	aaacctgtgg	2880
gcctcagtct	acagcagccg	caagatgctg	tttgcgttgc	cccacacgga	ccaggtcagt	2940
ggcctttgc	gtgccagctt	cctgctggcc	cagcagcgtc	tgctggagga	ccgcaaggac	3000
gttgtggtc	tggtaatcct	gagccctgac	gcccgcgtt	cccggttacgt	gcggctgcgc	3060
cagcgctct	gcccgcagag	tgtccttc	tggcccccacc	agcctagttgg	ccagcgcagc	3120
ttctgggccc	agctaggcat	ggccctgacc	aggacaacc	gccacttcta	taaccagaac	3180
ttctgcggg	gcccgcacgt	ggctgagtag	cacagagtga	cagcctggca	tgtacaaccc	3240
ccagccctga	ccttgcctct	ctgcctatga	tgcccagtct	gcctcactct	gtgacgcccc	3300
tgctctgcct	ccgcccaccc	cacccctggc	atacagcagg	caactaataa	atgcacttgg	3360
caggccaaac	agccaaaaaa	aaaaaaaaaa	a			3391

<210> 16
 <211> 2460
 <212> DNA
 <213> *Equus caballus*

<400> 16	atggccctt	gccatggtgc	cctgcagccc	ctgtctctcc	tgggcaggc	ggccatgctg	60
	ggcgtggc	tcggccaaagg	caccctgc	cctttcctgc	cctgtgagct	ccagccccac	120
	ggcctggta	actgcaactg	gctgttcc	aagtccgtgc	cccacttctc	agcagcagca	180
	ccccggaca	atgtcaccag	ccttccttg	ctctccaacc	gcatccacca	cctccacgac	240
	tccgactttg	cccaactgtc	caacctgcag	aaactcaacc	tcaaattggaa	ctgcccggca	300
	gccccctca	gccccatgca	cttcccgtc	cacatgacca	tcgagcccaa	cacttcctg	360
	gctgtaccca	ccctggagga	gctgaacctg	agctacaacg	gcatcacgac	tgtgcctgccc	420
	ctgcccagct	ccctcgtgtc	cctgtatc	agccgcacca	acatcctgca	gctagacccc	480
	accagcctca	cgggcctgca	tgccctgccc	ttccatataca	tggatggcaa	ctgctactac	540
	aagaacccct	gccccgggc	cctggaggtg	gccccaggcg	cccttccttg	cctggcaac	600
	ctcaccacc	tgtcactcaa	gtacaacaac	ctcacaacgg	tgcccccgcag	cctgccccct	660
	agcctggagt	acctgctgtt	gtcctacaac	cacattgtca	ccctggcacc	tgaggacctg	720
	gccaatctga	ctgcccgtc	tgtgcgtat	gtgggtggaa	actgcccggc	ctgtgaccat	780
	gcacgcaacc	cctgcgtgga	gtgcccacat	aaattccccc	agctgcactc	cgacaccc	840

agccaccta a gcccctaga aggccctcg t tgaaggata gttctctcta ccagctgaac	900
cccagatgg tccgtggcct gggcaacc c acagtgc tgc acctgagtga gaacttcctc	960
tacgactgca tcacccaaac caaggcatc cagggcctgg cccagctg c aagactcaac	1020
ttgtccttca attaccataa gaaggtgtcc ttcgcccacc tgacgctggc accctcc ttc	1080
gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttccg ctcactc a g c	1140
cagaagacgc tccagccact ggcccgc tgc cccatgctcc agcgtctgta tctgc a gat g	1200
aacttcatca accaggccca gtcggc a ttc aaggact tccctgg tct gctacata	1260
gacctgtc a gcaaccgc a c a c a c g c a t c a g t g g a g c t g t g g a g c c c a c a g g a g g t g	1320
gatgg tgg a g a a g g t c t g g c t a c a g a t c c a g g a c t c a c t c a g g c a c c a c	1380
cccagctcg aggacttcat gccaagctgc aagaacctca gttcacctt ggacctgtca	1440
c g g a a c a a c c t g g t a a c a g t c a c a g a g a t g t t t g c c c a g g c a g t g c	1500
c t g c g c t g a g c c a a c a c a g a t c g a g g c t g a g t g t c a c a g a t g t g c	1560
a c c a g c t g c a g g t g c t g g a c c t g c a g g c t g a g t g t a c c a t g a	1620
t t t a c g g a g c t g c a g g c t g a c t g g a g c t g a c t g a c a c a g g c a a c a c a g g c	1680
a t g c g g g t g t g g c a c a a c t c a g g c t t t g t g c c a c g c t g c a c c t a c t c	1740
a g c c t g g c a c a c a t g g c a c a g c t g c a g g c t g c a g g c t g c a c c t a t	1800
t g g g c c t g g a c t t c a g c g g a c a t t c c t g c a g g a t g t g a g g g a g a c c t c t a t	1860
c t c c g c t t c t t c a a g g c c t g a g a a g c c t a a t c c g g c t a g a c t g c a c c t a t	1920
c a t a c c t c c t g c a c c t g g c a a c c t c c a a g a g c c t g c a g g c t g c t c	1980
c g t a a c a a t t a c t g g c t t c t a a t t g g a c g c t g a c a c t g c t g c a c c t a t	2040
a c c c t g g a c c t g g a a a c c a g t g a a g g c t g a a g g c a g c c t g c a c c t a t	2100
a c c c a g c t c c a g g g c t g g a c g c t g a a g g c a g c c t g c a c c t a t	2160
t t t g c t c t g g a c a c g a g g c t g c a g g c t g c a c c t a t	2220
g a g c c t c t t g t t t c t a g c a g g c t g c a g g c t g c a c c t a t	2280
c c t c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t	2340
g t g c c t g g t c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t	2400
a t c t t c g c a c a a g a c c t g c g c t g c a c t g c a c t g c a c t g c a c t g c a c t g c a c t	2460

<210> 17
 <211> 1029
 <212> PRT
 <213> Ovis aries

<400> 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930

935

940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala
995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
1010 1015 1020

Gly Pro Thr Thr Ala Glu
1025

<210> 18
<211> 818
<212> PRT
<213> Ovis aries

<400> 18

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn		
115	120	125
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu		
130	135	140
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr		
145	150	155
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn		
165	170	175
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly		
180	185	190
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn		
195	200	205
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu		
210	215	220
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala		
225	230	235
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg		
245	250	255
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro		
260	265	270
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu		
275	280	285
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg		
290	295	300
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr		
305	310	315
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg		
325	330	335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly

<210>	19					
<211>	3199					
<212>	DNA					
<213>	Ovis aries					
<400>	19					
gtcggcacgg	gaagtgagcg	ccaagcatcc	ttccctgcag	ctgcccggca	acttgcccg	60
cagaccctct	ggagaagccg	cattccctgc	catggggccc	tactgtgcc	cgcacccccc	120
ttctctccctg	gtgcaggccg	cgccgcgtggc	agcagccctg	gcccagggca	ccctgcctgc	180
cttcctgccc	tgtgagctcc	agccccgggg	taaggtgaac	tgcaactggc	tgttcctgaa	240
gtctgtgcgg	cgcttttcgg	ccggagcccc	ccggggccaa	gtcaccagcc	tctcccttaat	300
ctccaaccgc	atccaccact	tgcacgactc	tgacttcgtc	cacctgtcca	acctgcgggt	360
cctcaaccc	aagtggaaact	gccccggccgc	cgccctcagc	cccatgcact	tcccctgcgg	420
catgaccatc	gagcccaaca	ccttcctggc	tgtccccacc	ctggaggagc	tgaacctgag	480
ctacaatggc	atcacgaccg	tgcctgcct	gcccagttct	ctcgatatccc	tgtcgctgag	540
ccgcaccaggc	atcctggtgc	taggccccac	ccacttcacc	ggcctgcacg	ccctgcgttt	600
tctgtacatg	gacggcaact	gttactataa	gaacccctgc	cagcaggccg	tggaggtggc	660
cccgaggccc	ctccctggcc	tggcaacct	cacgcacctg	tgcgtcaagt	acaacaaccc	720
cacggagggt	ccccggccgc	tgcctccctg	cctggacacc	ctgctgtgt	cctacaacca	780
catcatcacc	ctggcacccg	aggacctggc	caatctgact	gccctgcgtg	tgcttgatgt	840
gggcgggaac	tgccggccgt	gcaaccacgc	ccgcaacccc	tgcaggagc	gcccaaagaa	900
cttcccaag	ctgcaccctg	acacccctcg	ccacctgagc	cgccctgaaag	gcctgggttt	960
gaaggacagt	tctctctaca	aactagagaa	agactggttc	cgccggctgg	gcaggctcca	1020
agtgcgtcgc	ctgagtgaga	acttcctcta	tgactacatc	accaagacca	ccatccatcg	1080
gaacctgacc	cagctgcgca	gactcaaccc	gtccttcaat	taccacaaga	aggtgtcctt	1140
cgcacccac	caactggcac	cctcccttgg	gggcctggtg	tccctggaga	agctggacat	1200
gcacggcata	ttcttcggct	ccctcaccaa	caccacgctc	cgcccgctga	cccagctgcc	1260
caagctccag	agtctgagtc	tgcagctgaa	cttcatcaac	caggccgagc	tcagcatctt	1320
tggggccttc	ccgagcctgc	tcttcgtgga	cctgtcgac	aaccgcata	gcggagctgc	1380
gaggccggtg	gccgcctcg	gggaggtgga	cagcggggtg	gaagtctggc	ggtgcccccag	1440

gggcctcgct ccaggccccgc tggccgcccgt cagcgcaaag gacttcatgc caagctgcaa	1500
cctcaacttc accttggacc tgtcacggaa caaccctggtg acgatccagc aggagatgtt	1560
tacccgcctc tcccgccctcc agtgcctgctg cctgagccac aacagcatct cgcaggcggt	1620
taatggctcg cagttcgtgc cgctgaccccg cctgcgagtg ctcgacctgt cctacaacaa	1680
gctggacctg taccatgggc gctcggtcac ggagctgccc cagctggagg cactggacct	1740
cagctacaac agccagccct tcagcatgca gggcgtggc cacaacctca gcttcgtggc	1800
ccagctgccc tccctgcgct acctcagccct tgccacaaac ggcacccaca gccgcgtgtc	1860
acagaagctc agcagcgcct cgctgcgcgc cctggacttc agcggcaact ccctgagcca	1920
gatgtgggcc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctggtcca	1980
gctggacctg tccaagaacc acctgcacac ctcctgcct cgtcacctgg ataacctgcc	2040
caagagccctg cgccagctgc gtctccggga caataacctg gccttcttca actggagcag	2100
cctgactgtt ctgccccagc tggaagccct ggatctggcg ggaaaccagc tgaaggccct	2160
gagcaacggc agcctgccac ctggcaccccg gtcggcagaag ctggacgtga gcagcaacag	2220
catcggtttt gtgacccttg gtttcttctg cttgccaac cggctgaaaag agcttaacct	2280
cagcgccaaac gccctgaaga cagtgatcc cttctggttc ggtcgcttaa cagagaccct	2340
gaatatccctt gacgtgagcg ccaacccgct ccactgtgcc tgccccccgg cctttgtgga	2400
cttcctgtg gagatgcagg cggccgtgcc tggctgtcc aggcgcgtca cgtgtggcag	2460
tccggccag ctccaggggcc gcagcattt cgcacaggac ctgcgcctct gcctggatga	2520
gaccctctcc ttggactgtt ttggcttctc gctgctaattt gtggcgctgg gcctggcggt	2580
gccccatgtt caccacctctt gtggctggga cctgtggtaac tggctccacc tgtgtctggc	2640
ccatttgtccc cgacggcgcc ggcagccccgg cgaggacacc ctgtctacg atgccttcgt	2700
ggtcttcgac aaggcgcaga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca	2760
gctggaggag cgccgcgggc gcccggcgct ccgcctctgc ctggaggagc gagactggct	2820
ccctggcaag acgctttcg agaacctgtg ggctcggtc tacagcagcc gtaagaccat	2880
tttcgtgtt gaccacacgg accgggtcag tggctcctg cgcgcctactt tcctgtggc	2940
ccagcagcgc ctgttggagg accgcaagga tgctcggtg ctgggtatcc tgccggccgc	3000
cgcctaccgg tcccgctacg tgccggctgcg ccagcgccctc tgccgcaga gcgtccctct	3060
ctggccccac cagcccagtg gccaggtag ctctggcc aacctggca tggccctgac	3120
cagggacaac cgccacttcttataacccggaa ctctgcggg ggccccacga cagccgaata	3180

gcacagagtg	actgcccag	3199
------------	-----------	------

<210> 20		
<211> 2454		
<212> DNA		
<213> Ovis aries		
 <400> 20		
atggggccct actgtgcccc gcaccccttt tcttcctgg tgcaggccgc ggcgctggca	60	
gcagccctgg cccagggcac cctgcctgcc ttctgcctt gtgagctcca gccccgggt	120	
aaggtaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagccccc	180	
cgggccaatg tcaccagcct ctcccttaatc tccaaaccgca tccaccactt gcacgactct	240	
gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgcggcc	300	
ggcctcagcc ccatgcactt cccctgccgc atgaccatcg agcccaacac cttcctggct	360	
gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgcctg	420	
cccaggcttc tctgtatccct gtcgctgagc cgcaccagca tcctgggtct aggccccacc	480	
cacttcaccg gcctgcacgc cctgcgttt ctgtacatgg acggcaactg ctactataag	540	
aaccctgcc agcaggccgt ggaggtggcc ccaggcgccc tccttggct gggcaacctc	600	
acgcacctgt cgctcaagta caacaacctc acggaggtgc cccgcgcct gccccccagc	660	
ctggacaccc tgcgtgtgtc ctacaaccac atcatcaccc tggcacccga ggacctggcc	720	
aatctgactg ccctgcgtgt gcttgatgtg ggccggact gccgcgcgt cgaccacgccc	780	
cgcaacccct gcagggagtg cccaaagaac ttccccaagc tgcaccctga caccttcagc	840	
cacctgagcc gcctcgaagg cctgggttt aaggacagtt ctctctacaa actagagaaa	900	
gactggttcc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa cttcctctat	960	
gactacatca ccaagaccac catcttcagg aacctgaccc agctgcgcag actcaacctg	1020	
tccttcaatt accacaagaa ggtgtccttc gcccacctgc aactggcacc ctcccttggg	1080	
ggcctgggtgt ccctggagaa gctggacatg cacggcatct tcttccgcct cctcaccaac	1140	
accacgctcc gggcgcgtac ccagctgccc aagctccaga gtctgagttc gcagctgaac	1200	
ttcatcaacc aggccgagct cagcatctt gggcccttc cgagcctgtct ttcgtggac	1260	
ctgtcgaca accgcacatcg cggagctgctg aggccgggtgg cccgcctcgg ggaggtggac	1320	
agcgggggtgg aagtctggcg gtggccagg ggctcgctc caggcccgtt ggccgcgtc	1380	
agcgcaaagg acttcatgcc aagctgcaac ctcaacttca cttggacact gtcacggaac	1440	
aacctggta cgatccagca ggagatgttt acccgctct cccgcctcca gtgcctgcgc	1500	

ctgagccaca acagcatctc gcaggcggtt aatggctgc agttcgtgcc gctgaccgc 1560
 ctgcgagtgc tcgacactgtc ctacaacaag ctggacctgt accatggcg ctcgttcacg 1620
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680
 ggcgtggcc acaacactcg cttcgtggcc cagctgccgt ccctgcgcta cctcagcctt 1740
 gcgacacaacg gcatccacag ccgcgtgtca cagaagctca gcagcgcctc gctgcgcgccc 1800
 ctggacttca gcggcaactc cctgagccag atgtggcccg agggagacct ctatctctgc 1860
 ttcttcaaag gctttaggaa cctgggtccag ctggacctgt ccaagaacca cctgcacacc 1920
 ctcctgcctc gtacacttggaa taacactgccc aagagcctgc ggcagctgcg tctccggac 1980
 aataacactgg cttctttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg 2040
 gatctggccgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccgg 2100
 ctccagaagc tggacgtgag cagcaacagc atcggctttg tgacccttgg cttctttgtc 2160
 cttgccaacc ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220
 ttctggttcg gtcgcttaac agagaccctg aatatcctag acgtgagcgc caacccgctc 2280
 cactgtgcct gcggggccggc ctttggac ttcctgctgg agatgcagggc ggccgtgcct 2340
 gggctgtcca ggcgcgtcac gtgtggcagt ccggccagc tccagggcccg cagcatctc 2400
 gcacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21
 <211> 1032
 <212> PRT
 <213> Canis familiaris

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545	550	555	560
Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu			
565		570	575
Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg			
580		585	590
Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser			
595		600	605
Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg			
610		615	620
Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn			
625		630	635
Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser			
645		650	655
Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp			
660		665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly			
675		680	685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln			
690		695	700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro			
705		710	715
720			
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala			
725		730	735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly			
740		745	750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys			
755		760	765
-			
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro			
770		775	780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Ala Val Ala Leu Ser Leu
820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys
835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly
850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Leu Val Ile Leu Cys Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala
1025 1030

<210> 22
<211> 822
<212> PRT
<213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His His Leu His Asp
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro
545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu
565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg
580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser
595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg
610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn
625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser
645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660

665

670

Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly
 675 680 685

Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln
 690 695 700

Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro
 705 710 715 720

Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala
 725 730 735

Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly
 740 745 750

Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys
 755 760 765

Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro
 770 775 780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
 805 810 815

Ser Trp Val Cys Phe Ser
 820

<210> 23
 <211> 3334
 <212> DNA
 <213> Canis familiaris

<400> 23	
aggaaggggc tgtgagctcc aagcatccctt tcctgcagct gctgcccagc ctgccagcca	60
gaccctctgg agaagcccccc gctccctgtc atggcccccct gccgtggcgc cctgcacccc	120
ctgtctctcc tgggtgcaggc tgccgcgcta gcccggccc tggcccaggg caccctgcct	180
gccttcctgc cctgtgagct ccagccccat ggcctggtga actgcaactg gctgttcctc	240
aagtccgtgc cccgcttctc ggcagctgca ccccgcggtta acgtcaccag ctttccttg	300

tactccaacc	gcatccacca	cctccatgac	tatgactttg	tccacttgt	ccacctgcgg	360
cgtctcaatc	tcaagtggaa	ctgcccgc	gccagcctca	gccccatgca	ctttccctgt	420
cacatgacca	ttgagccaa	cacccctctg	gctgtgccc	ccctagagga	cctgaatctg	480
agctataaca	gcatcacgac	tgtgcccgc	ctgcccagtt	cgcttgtgtc	cctgtccctg	540
agccgcacca	acatccctgg	gctggaccc	gccaccctgg	caggcctta	tgcctgcgc	600
ttcctgttcc	tggatggcaa	ctgctactac	aagaacccct	gccagcaggc	cctgcagg	660
gccccaggtg	ccctcctggg	cctggcaac	ctcacacacc	tgtcactcaa	gtacaacaac	720
ctcaccgtgg	tgccgcgggg	cctgcccc	agcctggagt	acctgctt	gtcctacaac	780
cacatcatca	ccctggcacc	tgaggacctg	gccaatctga	ctgccc	tgcctcgat	840
gtgggtggga	actgtcgccg	ctgtgaccat	gcccgttaacc	cctgcagg	gtgccccaa	900
ggcttcccc	agctgcaccc	caacacc	ggccacctga	gccac	aggcctgg	960
ttgagggaca	gctctctcta	cagcctggac	cccagg	tccatgg	ggcaac	1020
atggtgctgg	acctgagtga	gaactt	cctg	tatgactgca	tcaccaa	1080
tacggcctgg	cccggtcg	cagactcaac	ctgtc	ttca	attatcataa	1140
tttgcccacc	tgc	atctggc	atc	ccttc	gggagc	1200
atacatggca	tcttcttccg	ctcg	ctc	agc	tccagtc	1260
cccatgctcc	agcgtctgca	tctgc	agtt	atca	gccagg	1320
ttcggcgcct	tccctggact	gcgg	gtac	gactt	gtcag	1380
gcagagcccg	cgg	ctg	ccac	ttt	ggact	1440
cagtcccg	ac	tt	gg	act	gtt	1500
agctgcagga	cc	ct	ca	tt	gtt	1560
ccggagatgt	tt	gt	cc	gg	ct	1620
tcgcaggcgg	tca	at	gg	ct	gc	1680
tcccataaca	ag	ct	gg	ac	tt	1740
gccttggacc	tca	g	ct	ac	aa	1800
agctttgtgg	cac	ag	ct	gg	cc	1860
agccgcgtgt	ccc	ag	cg	cc	tt	1920
accctgagcc	ag	at	gt	gg	cc	1980
agcctggttc	ag	ct	gg	ac	tt	2040
gacaacctcc	cc	aa	ag	gc	cc	2100
cca	ag	ag	gc	ct	cc	
cc	gg	gt	cc	ct	gt	
cc	gg	ct	cc	gt	gg	
cc	aa	tt	ac	cc	tt	
cc	aa	tt	ac	cc	tt	

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag	2160
ctgaaggccc ttagcaatgg cagcttgcac aacggcaccc agctccagag gctggacctc	2220
agcggcaaca gcatcggttt cgtggtcccc agctttttg ccctggccgt gaggcttcga	2280
gagctcaacc tcagcgccaa cgccctcaag acggtgagc cctcctggtt tggttccctg	2340
gcgggtgccc tgaaaagtctt agacgtgacc gccaacccct tgcattgcgc ttgcggcgca	2400
accttcgtgg acttcttgct ggaggtgcag gctgcggtgc ccggcctgcc tagccgtgtc	2460
aagtgcggca gcccgggcca gctccagggc cgccagcatct tcgcacagga cctgcgcctc	2520
tgcctggacg aagcgctctc ctgggtctgt ttcagcctct cgctgctggc tgtggccctg	2580
agcctggctg tgcccatgtc gcaccagctc tgtggctggg acctctggta ctgcttccac	2640
ctgtgcctgg cctggctgcc ccggcggggg cgccggcggg gtgtggatgc cctggcctat	2700
gacgccttcg tggcttcga caaggcgcag agctcggtgg cggactgggt gtacaatgag	2760
ctgcgggtac agctagagga ggcgcgtggg cgccgggcgc tacgcctgtg tctggaggaa	2820
cgtgactggg taccggcaa aaccctttc gagaacctct gggcctcagt ttacagcagc	2880
cgcaagacgc tgtttgcgt ggccgcacg gacagagtca gccgcctcct gcgtgccagc	2940
ttcctgtgg cccaaacagcg cctgctggag gaccgcagg acgtcgtggt gctggtgatc	3000
ctgtgcctgg acgcccaccc ctccgcata gtgcggctgc gccagcgcct ctgcgcctc	3060
agtgtcctcc tctggcccca ccagcccagt ggccagcgca gcttctggc ccagctggc	3120
acggcctga ccagggacaa ccgcaccc tacaaccaga acttctgcgg gggcccccacg	3180
acagcctgat aggcagacag cccagcacct tgcgcctt acaccctgcc tgtctgtctg	3240
ggatgcccga cctgctggct ctacaccgcg gctctgtctc ccctacaccc agccctggca	3300
taaaggcgtacc gctcaataaa tgctgctggt agac	3334

<210> 24
 <211> 2466
 <212> DNA
 <213> Canis familiaris

<400> 24 atggggccctt gccgtggcgc cctgcacccct ctgtctctcc tggtgcaggc tgccgcgtat	60
gccctggccc tggcccaggc caccctgcct gccttcgtgc cctgtgagct ccagccccc	120
ggcctgggtga actgcaactg gctgttcctc aagtccgtgc cccgcttctc ggcagctgca	180
ccccgcggta acgtcaccag cctttcccttg tactccaacc gcatccacca cctccatgac	240
tatgactttg tccacttcgt ccacctgcgg cgtctcaatc tcaagtggaa ctgcccggcc	300

gccagccatca gccccatgca ctttccctgt cacatgacca ttgagcccaa cacccctcgt 360
gctgtgccc ccctagagga cctgaatctg agctataaca gcatcacgac tgtgcccggc 420
ctgcccagtt cgcttgcgtc cctgtccctg agccgcacca acatcctggt gctggaccct 480
gccaccctgg caggccttta tgccctgcgc ttccctgttcc tggatggcaa ctgctactac 540
aagaaccctt gccagcaggc cctgcaggtg gccccaggtg ccctccctggg cctgggcaac 600
ctcacacacc tgtcactcaa gtacaacaac ctcaccgtgg tgccgcgggg cctggccccc 660
agcctggagt acctgctctt gtcctacaac cacatcatca ccctggcacc tgaggacctg 720
gccaatctga ctgcccctgcg tgtcctcgat gtgggtggga actgtcgccg ctgtgaccat 780
gcccgttaacc cctgcaggga gtgccccaaag ggcttccccc agctgcaccc caacacccctc 840
ggccacctga gccacacccgta aggccctggtg ttgagggaca gctctcteta cagcctggac 900
cccaggtgg tccatggcct gggcaacccctc atggtgctgg acctgagtga gaacttcctg 960
tatgactgca tcacccaaac caaagccttc tacggcctgg cccggctgcg cagactcaac 1020
ctgtccttca attatcataa gaaggtgtcc tttgcccacc tgcatctggc atcctccctc 1080
gggagccctac tgtccctgca ggagctggac atacatggca tcttcttccg ctgcgtcagc 1140
aagaccacgc tccagtcgct ggcccacccctg cccatgctcc agcgtctgca tctgcagttg 1200
aactttatca gccaggccca gtcagcatc ttccggccct tccctggact gcggtacgtg 1260
gacttgcag acaaccgcat cagtggagct gcagagcccg cggctgccac aggggaggtt 1320
gaggcagact gtggggagag agtctggcca cagtcccggtt accttgcctt gggccactg 1380
ggcacccccc gtcagagggc cttcatggcg agctgcagga ccctcaactt caccttggac 1440
ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggctt ggcgcgcctc 1500
cagtcctgg gcctgagcca caacagcatc tcgcaggccg tcaatggctc gcagttcggt 1560
cctctgagca acctgcgggt gctggacccctg tccctataaca agctggacccctt gtaccacggg 1620
cgctcggtca cggagctgcc gcggctggag gccttggacc tcagctacaa cagccagccc 1680
ttcagcatgc gggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc 1740
tacctcagcc tggcgcacaa tggcatccac agccgcgtgt cccagcagct ccgcagcgcc 1800
tcgctccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgagggagac 1860
ctctatctcc gcttcttcca aggcctgaga agcctgggtt acgtggacccctt gtcccagaat 1920
cgccctgcata ccctcctgcc acgcaacccctg gacaacccctcc ccaagagccct gcggccctcg 1980
cggtcccggt acaattacccctt ggccttttcc aactggagca gcctggccctt cctacccaaq 2040

ctggaagccc	tggacctggc	gggaaaccag	ctgaaggccc	tgagcaatgg	cagcttgc	ccc	2100
aacggcaccc	agctccagag	gctggaccc	agcggcaaca	gcatggctt	cgtggtccc	cc	2160
agctttttg	ccctggccgt	gaggctcga	gagctcaacc	tcagcgccaa	cgc	cctcaag	2220
acggtgaggc	cctcctggtt	tggccctg	gcgggtgccc	tgaaagtct	agacgtgacc	2280	
gccaaccct	tgcattgcgc	ttgcggcgca	acttcgtgg	acttcttgct	ggaggtgcag	2340	
gctgcggtgc	ccggcctgcc	tagccgtgc	aagtgcggca	gcccgggcca	gctccagg	gc	2400
cgcagcatct	tcccacagga	cctgcgcctc	tgctggacg	aagcgcttc	ctgggtctgt	2460	
ttcagc							2466

<210> 25
 <211> 1031
 <212> PRT
 <213> *Felis catus*

<400> 25

Met	Gly	Pro	Cys	His	Gly	Ala	Leu	His	Pro	Leu	Ser	Leu	Leu	Val	Gln
1															
															15

Ala	Ala	Ala	Leu	Ala	Val	Ala	Leu	Ala	Gln	Gly	Thr	Leu	Pro	Ala	Phe
20															30

Leu	Pro	Cys	Glu	Leu	Gln	Arg	His	Gly	Leu	Val	Asn	Cys	Asp	Trp	Leu
35															45

Phe	Leu	Lys	Ser	Val	Pro	His	Phe	Ser	Ala	Ala	Ala	Pro	Arg	Gly	Asn
50															60

Val	Thr	Ser	Leu	Ser	Leu	Tyr	Ser	Asn	Arg	Ile	His	His	Leu	His	Asp
65															80

Ser	Asp	Phe	Val	His	Leu	Ser	Ser	Leu	Arg	Arg	Leu	Asn	Leu	Lys	Trp
	85														95

Asn	Cys	Pro	Pro	Ala	Ser	Leu	Ser	Pro	Met	His	Phe	Pro	Cys	His	Met
									100						110

Thr	Ile	Glu	Pro	His	Thr	Phe	Leu	Ala	Val	Pro	Thr	Leu	Glu	Glu	Leu
	115														125

Asn	Leu	Ser	Tyr	Asn	Ser	Ile	Thr	Thr	Val	Pro	Ala	Leu	Pro	Ser	Ser
	130														140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe

610

615

620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Gly Ala Asp
850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala
865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu
930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser
965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu
980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe
1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu
1025 1030

<210> 26
<211> 820
<212> PRT
<213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Ala Phe Gln Gly Leu Ala Gln Leu
325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725

730

735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
 740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
 805 810 815

Asp Cys Phe Gly
 820

<210> 27
 <211> 3235
 <212> DNA
 <213> Felis catus

<400> 27						
agggtctgct	agctccaggc	attcttctct	gccatcgctg	cccagtctgc	catccagacc	60
ctctggagaa	gccccccactc	cctgtcatgg	gcccctgcca	tggcgccctg	cacccctgt	120
ctctcctgg	gcaggctgcc	gcgctggccg	tggccctggc	ccagggcacc	ctgcctgcct	180
ttctgcctg	ttagctccag	cgccacggcc	tggtaattt	cgactggctg	ttcctcaagt	240
ccgtgcccc	cttctcgccg	gcagcgcccc	gtggtaacgt	caccaggcctt	tccctgtact	300
ccaaccgc	ccaccacctc	cacgactccg	actttgtcca	cctgtccagc	ctgcggcg	360
tcaaccta	atggaaactgc	ccacccgcca	gcctcagccc	catgcacttc	ccctgtcaca	420
tgaccattg	gccccacacc	ttcctggccg	tgcccaccc	ggaggagctg	aacctgagct	480
acaacagca	cacgacagta	cccgccctgc	ccagttccct	cgtgtccctg	tccttgagcc	540
gtaccaacat	cctggtgctg	gaccctgcca	acctcgagg	gctgcactcc	ctgcgtttc	600
tgttcctg	tggcaactgc	tactacaaga	accctgccc	gcaggccctg	caggtggccc	660
cgggcgc	ccttggcctg	ggcaaccta	cgcacctgtc	actcaagtac	aacaacctca	720
ctgcggtgcc	ccgcggcctg	ccccccagcc	tggagtacct	gttattgtcc	tacaaccaca	780

tcatcacccct	ggcacacctgag	gacctggcca	acctgaccgc	cctgcgtgtg	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	geaacccttg	tatggagtgc	cccaagggct	900
tcccgacccct	gcaccctgac	accttcagcc	acctgaacca	cctcgaaggc	ctgggtgtga	960
aggacagctc	tctctacaac	ctgaacccca	gatggttcca	tgccctgggc	aacctcatgg	1020
tgctggacct	gagtgagaac	ttccttatatg	actgcacac	caaaaccaca	gccttccagg	1080
gcctggccc	gctgcccaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtccttg	1140
cccacccgtca	tctggcgccc	tccttcggga	gcctgctctc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttccgctcg	ctcagcaga	ccacgctccg	gtcgctggtc	cacccgtcc	1260
tgctccagag	tctgcacccctg	cagatgaact	tcatcaatca	ggcccagctc	agcatcttcg	1320
gggccttccc	tggcctgcga	tacgtggacc	tgtcagacaa	ccgcataagt	ggagccatgg	1380
agctggcggc	tgccacgggg	gaggtggatg	gtggggagag	agtccggctg	ccatctgggg	1440
acctagctct	gggcccacccg	ggcaccccta	gctccgaggg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	cacccggac	ctgtcacgg	acaacccatgt	gacaatccag	ccagagatgt	1560
ttgcccggct	ctcgccctc	cagtgcctgc	tcctgagccg	caacagcata	tcgcaggcag	1620
tcaacggctc	acaattttatg	ccgctgacca	gcctgcaggt	gctggacactg	tccataaca	1680
agctggacct	gtaccatggg	cgctcttca	cgagactgccc	gcggctggag	gccctggacc	1740
tcagctacaa	cagccagccc	ttcagcatgc	agggcgtggg	tcacaaccc	agctttgtgg	1800
cacagctgcc	ggccctgcgc	tatctcagcc	tggcgcacaa	cgacatccac	agccgtgtgt	1860
cccagcagct	ctgcagcggcc	tcgctgcggg	ccttggactt	cagcggcaat	gccttgcagcc	1920
ggatgtgggc	cgagggagac	ctgtatctcc	acttcttccg	aggcctgagg	agcctggacc	1980
ggttggatct	gtcccagaat	cgccctgcata	ccctcttgc	acgcaccctg	gacaacctcc	2040
ccaagagcct	gcggctgctg	cgtctccgtg	acaatttatct	ggctttcttc	aactggagca	2100
gcctggctct	cctccccagg	ctggaagccc	tggacctggc	ggaaaccag	ctgaaggccc	2160
tgagcaacgg	cagcttgcct	aatggaaccc	agctccagag	gctggacctc	agcagcaaca	2220
gtatcagctt	cgtggcctcc	agcttttttg	ctctggccac	caggctgcga	gagctcaacc	2280
tcagtgccaa	cgcctcaag	acggtgagc	cctcctggtt	cggttctcta	gcgggcaccc	2340
tgaaaagtcc	agatgtgact	ggcaacccccc	tgcactgcgc	ctgtggggcg	gccttcgtgg	2400
acttcttgc	ggaggtgcag	gctgcagtgc	ccggcctgccc	aggccacgtc	aagtgtggca	2460
gtccaggtca	gctccagggc	cgcagcatct	ttgcgcagga	tctgcgcctc	tgcctggatg	2520
aggccctctc	ctgggactgt	tttggcctct	cgctgctgac	cgtggccctg	ggcctggccc	2580

tgcccatgct gcaccacac	tgtggctggg acctctggta	ctgcttccac	ctgtgcctgg	2640		
cctggctgcc	ccggcgaaaa	cgcgccggg	gcgcggatgc	cctgcctac	gatgccttg	2700
tggcttcga	caaggcacag	agcgccgtgg	ccgactgggt	gtacaacgag	ctgcgggtac	2760
ggctagagga	gcgcgtgga	cgccgagcgc	tccgcctgtg	cctggaggaa	cgtgactggc	2820
tacccgtaa	aacgctcttt	gagaacctgt	gggcctcagt	ttacagcagc	cgcaagatgc	2880
tgtttgtgct	ggcccacaca	gacagggtca	gccccctt	gcgccagc	tttctgctgg	2940
cccagcagcg	cctgctggag	gaccgcaagg	acgttgtgg	gctggtgatc	ctgcgccccg	3000
acgcccacccg	ctcccgctat	gtgcggctgc	gccagcgcct	ctgcccacag	agcgtccctcc	3060
tctggcccca	ccagccccagt	ggccagcgca	gcttctgggc	ccagctggc	acggccctga	3120
ccagggacaa	ccagcacttc	tataaccaga	acttctgccc	gggccccacg	acggcagagt	3180
gaccgcccag	caccccaagc	ctcctacacc	ttgcctgtct	gcctgggatg	ccggg	3235

<210> 28
 <211> 2460
 <212> DNA
 <213> *Felis catus*

<400> 28	atggggccct	gcacatggcgc	cctgcacccc	ctgtctctcc	tggtgcaggg	tgccgcgcgtg	60
	gccgtggccc	tggcccaggg	caccctgcct	gcctttctgc	cctgtgagct	ccagcgccac	120
	ggcctggta	attgcgactg	gctgttcctc	aagtccgtgc	cccacttctc	ggcggcagcg	180
	ccccgtggta	acgtcaccag	cctttccctg	tactccaacc	gcatccacca	cctccacgac	240
	tccgactttg	tccacctgtc	cagcctgcgg	cgtctcaacc	tcaaatggaa	ctgcccaccc	300
	gccagcctca	gccccatgca	cttcccctgt	cacatgacca	ttgagcccca	caccttcctg	360
	gccgtgccc	ccctggagga	gctgaacctg	agctacaaca	gcatcacgac	agtacccgac	420
	ctgcccagtt	ccctcgtgtc	cctgtccctg	agccgtacca	acatcctgg	gctggaccct	480
	gccaacctcg	cagggctgca	ctccctgcgc	tttctgttcc	tggatggcaa	ctgctactac	540
	aagaacccct	gcccgcaggc	cctgcaggtg	gccccggcgc	ccctccctgg	cctggcaac	600
	cttacgcacc	tgtcactcaa	gtacaacaac	ctcactgcgg	tgccccgcgg	cctgcccccc	660
	agcctggagt	acctgctatt	gtcctacaac	cacatcatca	ccctggcacc	tgaggacctg	720
	gccaacctga	ccgcccgtcg	tgtgctcgat	gtgggtggga	actgccgtcg	ctgtgaccac	780
	gcccgcaccc	cctgtatgga	gtgccccaa	ggcttcccgc	acctgcaccc	tgacaccc	840
	agccacacctg	accacacctg	aggcctggtg	ttgaaggaca	gtctctctca	caacacctgaa	900

cccagatgg	tccatgcct	ggcaaccc	atgggtctgg	acctgagtga	gaacttccta	960	
tatgactgca	tcacccaaac	cacagcc	caggcctgg	cccagctgcg	cagactcaac	1020	
ttgtcttca	attaccacaa	gaagggtgtcc	tttgc	ccatctggc	gcctccttc	1080	
gggagcctgc	tctccctgca	gcagctggac	atgc	atggc	tcttcttccg	1140	
gagaccacgc	tccgg	tcgct	ggtccac	ccatgtcc	agagtctgca	1200	
aacttcatca	atcaggccc	gctc	agc	atgc	cctgc	1260	
gac	ctgtc	ag	aa	ccgc	atgg	gagcc	1320
gatgg	tttgg	gg	ag	ggatcc	gtcc	ccatct	1380
cctag	ctccg	agg	gg	tttcat	gc	aggctgc	1440
cgga	acaacc	tagt	gaca	at	ccat	tttgc	1500
ctg	cct	ccg	caac	gc	ggc	atgtc	1560
acc	agc	ctgc	ccat	gg	ccat	tttgc	1620
ttc	acgg	gg	ccat	gg	ccat	tttgc	1680
atg	cagg	gg	gg	ccat	gg	ccat	1740
agc	ctgg	cc	ccat	gg	ccat	tttgc	1800
cgg	cctt	gg	ccat	gg	ccat	tttgc	1860
ctcc	actt	cc	ccat	gg	ccat	tttgc	1920
cata	ccct	cc	ccat	gg	ccat	tttgc	1980
cgt	acaatt	at	ctgg	ccat	tttgc	tttgc	2040
gc	ccttgg	gg	gg	ccat	gg	ccat	2100
accc	agc	tttgc	gg	ccat	gg	ccat	2160
tttgc	tct	cc	ccat	gg	ccat	tttgc	2220
gag	ccct	cc	ccat	gg	ccat	tttgc	2280
ccc	ctgc	cc	ccat	gg	ccat	tttgc	2340
gtg	cccg	cc	ccat	gg	ccat	tttgc	2400
atctt	tcgc	cc	ccat	gg	ccat	tttgc	2460

<210> 29
 <211> 1032
 <212> PRT
 <213> *Mus musculus*

<400> 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225	230	235	240
Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg			
245	250	255	
Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser			
260	265	270	
Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly			
275	280	285	
Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe			
290	295	300	
Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu			
305	310	315	320
Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu			
325	330	335	
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala			
340	345	350	
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu			
355	360	365	
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu			
370	375	380	
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met			
385	390	395	400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala			
405	410	415	
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr			
420	425	430	
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu			
435	440	445	
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser			
450	455	460	

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
1025 1030

<210> 30
<211> 821
<212> PRT
<213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340

345

350

Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu
370 375 380

Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr
420 425 430

Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu
435 440 445

Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser
450 455 460

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Ala Phe Val Asp Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
805 810 815

Trp Asp Cys Phe Gly
820

<210> 31
<211> 3200
<212> DNA
<213> Mus musculus

<400> 31	
tgtcagaggg agcctcggga gaatcctcca tctcccaaca tggttctccg tcgaaggact	60
ctgcacccct tgcacccct ggtacaggct gcagtgcgtgg ctgagactct ggcctgggt	120
accctgcctg ccttcctacc ctgtgagctg aagcctcatg gcctggtgga ctgcaattgg	180
ctgttcctga agtctgtacc ccgtttctct gcggcagcat cctgcctcaa catcaccgc	240
ctctccttga tctccaaaccg tatccaccac ctgcacaact ccgacttcgt ccacctgtcc	300
aacctgcggc agctgaacct caagtggAAC tggccaccca ctggccttag cccctgcac	360
ttctcttgcc acatgaccat tgagcccaga accttcctgg ctatgcgtac actggaggag	420
ctgaacctga gctataatgg tatcaccact gtgcggcgtac tgcccagctc cctggtaat	480
ctgagcctga gccacaccaa catcctgggtt cttagatgcta acagcctcgc cggcctatac	540
agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccctg cacaggagcg	600
gtgaagggtga ccccaggcgc cctcctggc ctgagcaatc tcacccatct gtctctgaag	660
tataacaacc tcacaaaggt gccccccaa ctgccccca gcctggagta cctcctggtg	720
tcctataacc tcattgtcaa gctgggcct gaagacctgg ccaatctgac ctcccttoga	780
gtacttgatg tgggtggaa ttgccgtgc tgccgaccatg ccccaatcc ctgtatagaa	840
tgtggccaaa agtccctcca cctgcacccct gagaccttc atcacctgag ccacatggaa	900
ggcctggcgc tgaaggacag ctctctccat acactgaact cttcctgggtt ccaaggctcg	960
gtcaacctct cggtgctgga cctaaggcag aactttctct atgaaagcat caaccacacc	1020
aatgccttc agaacctaac ccgcctgcgc aagctcaacc tgccttcaa ttaccgcaag	1080
aaggtagtcct ttgccccctt ccacctggca agttccttca agaacctgggt gtcactgcag	1140
gagctgaaca tgaacggcat cttcttcgc tgcgtcaaca agtacacgct cagatggctg	1200
gccgatctgc ccaaactcca cactctgcat cttcaaattga acttcatcaa ccaggcacag	1260
ctcagcatct ttggtagccctt ccgagccctt cgctttgtgg acttgtcaga caatcgcatc	1320
agtgggcctt caacgctgta agaagccacc cctgaagagg cagatgtgc agagcaggag	1380
gagctgttgtt ctgcggatcc tcacccagct ccactgagca cccctgttc taagaacttc	1440

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaaaca cctggtgact	1500
atcaagccag agatgtttgt caatctctca cgcctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttccctgccgc tgactaatct gcaggtgctg	1620
gacctgtccc ataacaaaact ggacttgtac cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacacctgag ctacaacacgc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc tttagcctggc acacaatgac	1800
attcataccct ggtgtccctc acatctcaac agcaactcag tgaggttct tgacttcagc	1860
ggcaacggta tggggccgcat gtgggatgag gggggccctt atctccattt cttccaaggc	1920
ctgagtgccgc tgctgaagct ggacctgtct caaaaataacc tgcatatcct ccggccccag	1980
aaccttgaca acctccccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtccttcctg cccaaacctgg aagtccctaga cctggcaggc	2100
aaccagctaa aggccctgac caatggcacc ctgcctaattt gcaccctctt ccagaaactg	2160
gatgtcagca gcaacagttt cgtctctgtgt gtcccagctt tcttcgtctt ggccgtcgag	2220
ctgaaagagg tcaacacctgag ccacaacattt ctcaagacgg tggatcgctc ctggtttggg	2280
cccatgtga tgaacctgac agttcttagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgttagactt actgttggag gtgcagacca aggtgcctgg cctggctaat	2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctcttttgg gactgttttgc gccttcactt cttggctgt	2520
gccgtggca tgggtgggcc tatactgcac catctctgcg gctggacgt ctggactgt	2580
tttcatctgt gcctggcatg gctaccttttgc ctggccgc gcccacgcg cggccaaact	2640
ctccctatg atgccttcgtt ggtgttcgtt aaggcacaga ggcgcgttgc ggactgggt	2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggc gcccggccct acgcttgcgt	2760
ctggaggacc gagattggctt gcctggccag acgcttttgc agaaccttcg ggcttcattc	2820
tatggagcc gcaagactctt atttgcgtt gcccacacgg accgcgttcag tggccttcgt	2880
cgcaccagct tcctgtggc tcagcagcgc ctgttggaaag accgcaagga cgtgggtgg	2940
ttgggtatcc tgcgtccgga tgcccaccgc tcccgctatg tgcgcactgcg ccagcgtctc	3000
tgcgcgcaga gtgtgtctttt ctggcccccag cagcccaacg ggcagggggg cttctggcc	3060
cagctgagta cagccctgac tagggacaac cgccacttctt ataaccagaa cttctgcgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcattt catgcctgg	3180
tccccagtttgc ctctgcctgc	3200

<210> 32
 <211> 2463
 <212> DNA
 <213> *Mus musculus*

<400> 32
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggcacaggc. tgcagtgctg 60
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120
 ggcctggtgg actgcaattg gctgttcctg aagtctgtac cccgtttctc tgcggcagca 180
 tcctgtcaca acatcacccg ccttccttg atctccaacc gtatccacca cctgcacaac 240
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300
 actggcctta gccccctgca cttctttgc cacatgacca ttgagcccg aaccccttcgt 360
 gctatgcgtt cactggagga gctgaacctg agctataatg gtatcaccac tgtggcccg 420
 ctgcccagct ccctggtgaa tctgagccctg agccacacca acatcctggt tctagatgct 480
 aacagcctcg cccgcctata cagcctgcgc gttctttca tggacgggaa ctgctactac 540
 aagaacccct gcacaggagc ggtgaaggtg accccaggcg ccctccctggg cctgagcaat 600
 ctcacccatc tgtctctgaa gtataacaac ctcaccaaagg tgccccggca actgcccccc 660
 agcctggagt acctccctggt gtcctataac ctcattgtca agctggggcc tgaagacctg 720
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780
 gcccccaatc cctgtataga atgtggccaa aagtccctcc acctgcaccc tgagaccttc 840
 catcacctga gccatctgga aggcctggtg ctgaaggaca gctctctcca tacactgaac 900
 tttccctggt tccaagggtct ggtcaacctc tcggtgctgg acctaagcga gaactttctc 960
 tatgaaagca tcaaccacac caatgcctt cagaacctaa cccgcctgcg caagctcaac 1020
 ctgtccttca attaccgcaa gaaggatgcc tttgcccggc tccacctggc aagttccttc 1080
 aagaacctgg tgtcaactgca ggagctgaac atgaacggca ttttcttccg ctcgctcaac 1140
 aagtacacgc tcagatggct ggccgatctg cccaaactcc acactctgca tcttcaaatg 1200
 aacttcatca accaggcaca gtcagcatc tttggatcc tccgagccct tcgccttgc 1260
 gacttgcag acaatcgcat cagtgccct tcaacgctgt cagaagccac ccctgaagag 1320
 gcagatgtatc cagagcagga ggagctgtg tctgcggatc ctcacccagc tccactgagc 1380
 accccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440
 tctcggaaaca acctgggtgac tatcaagcca gagatgttg tcaatctctc acgcctccag 1500
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctggcg 1560

ctgactaatac	tgcaggtgct	ggacctgtcc	cataacaaac	tggacttcta	ccactggaaa	1620
tcgttcagtg	agctaccaca	gttgcaggcc	ctggacactga	gctacaacag	ccagcccttt	1680
agcatgaagg	gtataggcca	caatttcagt	tttgtggccc	atctgtccat	gctacacagc	1740
cttagcctgg	cacacaatga	cattcatacc	cgtgtgtct	cacatctcaa	cagcaactca	1800
gtgaggtttc	ttgacttcag	cggtcaacgg	atggggcgca	tgtggatga	ggggggcctt	1860
tatctccatt	tcttccaagg	cctgagtgcc	ctgctgaagc	tggacctgtc	tcaaaataac	1920
ctgcatatcc	tccggccccca	gaaccttgac	aacctccccca	agagcctgaa	gctgctgagc	1980
ctccgagaca	actacctatac	tttcttaac	tggaccagtc	tgtccttcct	gcccaacactg	2040
gaagtcctag	acctggcagg	caaccagcta	aaggccctga	ccaatggcac	cctgcctaatt	2100
ggcacccctcc	tccagaaaact	ggatgtcagc	agcaacagta	tctgtctgt	ggtcccagcc	2160
ttcttcgctc	tggcggtcga	gctgaaagag	gtcaacactca	gccacaacat	tctcaagacg	2220
gtggatcgct	cctggtttgg	gcccattgtg	atgaacactga	cagttctaga	cgtgagaagc	2280
aaccctctgc	actgtgcctg	tggggcagcc	ttcgttagact	tactgttgg	ggtgcagacc	2340
aagggtgcctg	gcctggctaa	tgggtgtgaag	tgtggcagcc	ccggccagct	gcagggccgt	2400
agcatcttcg	cacaggacct	gcggctgtc	ctggatgagg	tccctctttt	ggactgcttt	2460
ggc						2463

<210> 33
 <211> 1032
 <212> PRT
 <213> Homo sapiens

 <400> 33

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

305

310

315

320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu
420 425 430

Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu
435 440 445

Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu
515 520 525

Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu
1025 1030

<210> 34
<211> 820
<212> PRT
<213> Homo sapiens

<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420

425

430

Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu
435 440 445

Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu
450 455 460

Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
485 490 495

His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu
515 520 525

Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
 805 810 815

Asp Cys Phe Ala
 820

<210> 35
 <211> 3352
 <212> DNA
 <213> Homo sapiens

 <400> 35
 aggctggat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtggaaag 60
 ggacctcgag tgtgaagcat cttccctgt agctgctgtc cagtctgccc gccagaccct 120
 ctggagaagc ccctgcccc cagcatgggt ttctgcccga gcccctgca cccgctgtct 180
 ctccctgggtc aggccatcat gctggccatg accctggccc tgggtacatt gcctgccttc 240
 ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc agcaccgcgt ggcaatgtca ccagctttc cttgtctcc	360
aaccgcatcc accacctcca tgattctgac tttgcccacc tgcccagcct gcggcatctc	420
aacctcaagt ggaactgccc gccggttggc ctcagccca tgcacttccc ctgcacatg	480
accatcgagc ccagcacctt cttggctgtg cccaccctgg aagagctaaa cctgagctac	540
aacaacatca tgactgtgcc tgcgctgccc aaatccctca tatccctgtc cctcagccat	600
accaacatcc tgatgctaga ctctgccagc ctcgcccggcc tgcattgcct ggcgttccta	660
ttcatggacg gcaactgtta ttacaagaac ccctgcaggc aggactgga ggtggccccc	720
gggtccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact	780
gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tggatgtccca caaccgcac	840
gtcaaaactgg cgcctgagga cctggccaaat ctgacccccc tgcgtgtgct cgatgtggc	900
ggaaattgcc gccgctgcga ccacgctccc aaccctgca tggagtgcctc tgcgtacttc	960
ccccagctac atcccgatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag	1020
gacagttctc tctcctggct gaatgccagt tggatccgtg ggctggaaa cctccgagtg	1080
ctggacactga gtgagaactt cctctacaaa tgcattacta aaaccaaggc cttccaggc	1140
ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagaggggt gtcctttgcc	1200
cacctgtctc tggcccttc cttcggagc ctggatccccc tgaaggagct ggacatgcac	1260
ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccg cctgcccatt	1320
ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg	1380
gccttcctg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag	1440
ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggatgca gcctggggac	1500
cttgctccgg ccccagtggc cactcccaggc tctgaagact tcaggccaa ctgcagcacc	1560
ctcaacttca cttggatct gtcacggAAC aacctggatc ccgtgcagcc ggagatgttt	1620
gcccagctct cgacactgca gtgcctgcgc ctgagccaca actgcatttc gcaggcagtc	1680
aatggctccc agttcctgccc gctgaccggc ctgcaggatgc tagacctgtc ccgcaataag	1740
ctggacactt accacgagca ctcattcacg gagctaccgc gactggaggc cctggacactc	1800
agctacaaca gccagccctt tggcatgcag ggcgtggcc acaacttcag cttcgatggct	1860
cacccatgcgc cccatgcgc cctcagccctg gcccacaaca acatccacag ccaagtgtcc	1920
cagcagctct gcagttacgtc gctgcggcc ctggacttca gcccgtatgc actggccat	1980
atgtggcccg agggagaccc ctatctgcac ttcttccaag gcctgaggcgg tttgatctgg	2040

ctggacttgt	cccagaaccg	cctgcacacc	ctcctgcccc	aaaccctgcg	caacccccc	2100
aagagcctac	aggtgctgcg	tctccgtgac	aattacctgg	catttttaa	gtggggagc	2160
ctccacttcc	tgcccaaact	ggaagtcc	gacctggcag	gaaaccggct	gaaggccctg	2220
accaatggca	gcctgcctgc	tggcacccgg	ctccggaggc	tggatgtcag	ctgcaacagc	2280
atcagcttcg	tggcccccgg	cttctttcc	aaggccaagg	agctgcgaga	gctcaacctt	2340
agcgccaaacg	ccctcaagac	agtggaccac	tcctggtttgc	ggcccccggc	gagtgcctg	2400
caaatactag	atgtaagcgc	caaccctctg	cactgcgcct	gtggggccgc	ctttatggac	2460
ttccctgctgg	aggtgcagggc	tgccgtgccc	ggtctgccc	gccgggtgaa	gtgtggcagt	2520
ccggggccagc	tccagggcct	cagcatctt	gcacaggacc	tgegcctctg	cctggatgag	2580
gccctctcct	gggactgttt	cgcgcctctg	ctgctggctg	tggctctggg	cctgggtgtg	2640
cccatgctgc	atcacctctg	tggctggac	ctctggta	gcttccac	gtgcctggcc	2700
tggctccct	ggcgggggcg	gcaaagtggg	cgagatgagg	atgcctgccc	ctacgatgcc	2760
ttcgtgtct	tcgacaaaac	gcagagcga	gtggcagact	gggtgtacaa	cgagttcgg	2820
gggcagctgg	aggagtgccc	tggcgctgg	gcactccgccc	tgtgcctgga	ggaacgcgac	2880
tggctgcctg	gcaaaaccct	ctttgagaac	ctgtggccct	cggctatgg	cagccgcaag	2940
acgctgtttg	tgctggccca	cacggaccgg	gtcagtggtc	tctgcgcgc	cagcttcctg	3000
ctggcccagc	agcgccctgct	ggaggaccgc	aaggacgtcg	tggtgcgtgt	gatcctgagc	3060
cctgacggcc	gccgcctcccg	ctacgtgcgg	ctgcgcctgc	gcctctgccc	ccagagtgtc	3120
ctcctctggc	cccaccagcc	cagtggtcag	cgcagcttct	gggcccagct	gggcatggcc	3180
ctgaccaggg	acaaccacca	cttctataac	cgaaacttct	gccagggacc	cacggccgaa	3240
tagccgtgag	ccgaaatcct	gcacggtgcc	acotccacac	tcacctcacc	tctgcctgcc	3300
tggtctgacc	ctccctgtct	cgcctccctc	accccacacc	tgacacagag	ca	3352

<210> 36
 <211> 2460
 <212> DNA
 <213> Homo sapiens

<400> 36						
atgggtttct	gccgcagcgc	cctgcaccccg	ctgtctctcc	tggtgcagggc	catcatgctg	60
gccatgaccc	tggccctggg	taccttgccc	gccttcctac	cctgtgagct	ccagccccac	120
ggcctggta	actgcaactg	gctgttcctg	aagtctgtgc	cccacttctc	catggcagca	180
ccccgtggca	atgtcaaccag	ccttccttg	tcctccaacc	gcatccacca	cctccatgat	240

tctgactttg	ccacacctgcc	cagcctgcgg	catctcaacc	tcaagtggaa	ctgcccggcg	300	
gttggcctca	gccccatgca	cttccctgc	cacatgacca	tcgagcccag	caccttcttg	360	
gctgtgccc	ccotggaaaga	gctaaacctg	agctacaaca	acatcatgac	tgtgcctgcg	420	
ctgccc	aaat	ccotcatatc	cctgtccctc	agccatacca	acatcctgat	480	
gccagcctcg	ccggcctgca	tgccctgcgc	ttcctattca	tggacggcaa	ctgttattac	540	
aagaacccct	gcaggcaggc	actggaggtg	gccccgggtg	ccctccttgg	cctgggcaac	600	
ctcacc	cacc	tgtcactcaa	gtacaacaac	ctcactgtgg	tgcccccga	660	
agcctggagt	atctgctgtt	gtcctacaac	cgcacatgtca	aactggcgcc	tgaggacctg	720	
gccaatctga	ccgccc	tgc	tgtgctcgat	gtggggcggaa	attgccgcg	780	
gctcccaacc	cctgc	atgga	gtgcatgga	gtgcctcg	cacttcccc	840	
agccac	cctg	actg	gccccttga	aggcctggtg	ttgaaggaca	900	
gccagttgg	tccgtgg	gtt	ggaaacctc	cgagtgctgg	acctgagtga	960	
tacaaatgca	tcact	aaac	caaggcc	caggcctaa	cacagctgcg	1020	
ctgtc	ccttca	attac	aaaa	gagggtgtcc	tttgc	cccttc	1080
gggagc	ctgg	tcg	ccctgaa	ggagctggac	atgcacggca	tcttcttcc	1140
gagaccac	gc	tcc	ggccact	ggccgc	cctgc	ccatgctcc	1200
aacttcatca	accagg	ccca	gtcggc	atc	tcagg	ccctggc	1260
gac	tcgg	aca	accgc	cat	cgag	ctgta	1320
gatggagg	gg	aga	agg	tctg	gtcag	cccttgc	1380
cccag	ctctg	aag	acttc	actgc	acttc	ccat	1440
cgg	aca	acc	ttc	actgc	acttc	ccat	1500
ctgc	gcct	gca	act	tcg	ccat	gtgc	1560
acc	gg	ttc	tcg	act	tcg	ccat	1620
ttc	acgg	gg	tcg	gg	tcg	ccat	1680
atgc	agg	gg	tcg	gg	tcg	ccat	1740
agc	ctgg	cc	aca	acat	ccat	gtgc	1800
cgg	ccct	gg	cc	atgc	atgt	ccat	1860
ctg	cactt	tc	caagg	cttgc	ttgc	ccat	1920
cac	ccct	cc	ttcagg	ccat	ttgc	ccat	1980
cgt	acaatt	ttt	acttgg	ttgg	ttgc	ccat	2040

gtcctcgacc tggcagggaaa ccggctgaag gccctgacca atggcagcct gcctgctggc 2100
acccggctcc ggaggctgga tgtcagctgc aacagcatca gcttcgtggc cccggcttc 2160
tttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgcctt caagacagtg 2220
gaccactcct ggtttgggccc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280
cctctgcact ggcctgtgg ggcggccccc atggacttcc tgctggaggt gcaggctgcc 2340
gtgccccggtc tgcccagccg ggtgaagtgt ggcagtcggg gccagctcca gggcctcagc 2400
atcttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 37
accttgcctg ctttcctacc ctgtga 26

<210> 38
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 38
gtccgtgtgg gccagcacaa a 21

<210> 39
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 39
tccatgacgt ttttgatgtt 20

<210> 40
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 40
tccataacgt ttttcatgtt

20

<210> 41
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 41
tccatcacgt ttttcatgtt

20

<210> 42
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 42
tccattacgt ttttcatgtt

20

<210> 43
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 43
tccatggcgt ttttcatgtt

20

<210> 44
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 44
tccatgccgt ttttcatgtt

20

<210> 45
<211> 20
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgtcgt ttttcatgtt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgtatgt ttttcatgtt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttcatgtt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttcatgtt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttcatgtt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 50
tccatgacct ttttgatgtt

20

<210> 51
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 51
tccatgactt ttttgatgtt

20

<210> 52
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 52
tccatgacgc ttttgatgtt

20

<210> 53
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 53
tccatgacga ttttgatgtt

20

<210> 54
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 54
tccatgacgg ttttgatgtt

20

<210> 55
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 55
tccatgacgt ct^{tt}gatgtt

20

<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 56
tccatgacgt at^{tt}gatgtt

20

<210> 57
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 57
tccatgacgt gt^{tt}gatgtt

20

<210> 58
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 58
tcgtcg^{tttt} gtcg^{tttt}gt cg^{tt}

24

<210> 59
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 59
tgctcg^{tttt} gtg^{tttt}gt g^{ttt}

24

<210> 60
<211> 20
<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 60

tccatgacgt tcctgatgct

20

<210> 61

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 61

tccatgagct tcctgatgct

20

<210> 62

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus oligopeptide

<220>

<221> MISC_FEATURE

<222> (4)..(5)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (7)..(12)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (14)..(15)

<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys
1 5 10 15

<210> 64
<211> 16
<212> PRT
<213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys
1 5 10 15

<210> 65
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Consensus oligopeptide

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

<210> 66
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

<210> 67
<211> 31
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (2)..(8)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(22)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(30)
<223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr
20 25 30

<210> 68
<211> 31
<212> PRT
<213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His
1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr
20 25 30

<210> 69
<211> 31
<212> PRT
<213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

1

5

10

15

Ser Phe Ser Glu Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr
20 25 30

<210> 70
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 70 20
tccaggactt ctctcagggtt